AAV86895 standard; cDNA, 471 BP.

4AV86895

(first entry)

27-APR-1999

AAV86895;

EST clone BM4.

lomo sapiens W09845435-A2 10-APR-1998; LO-APR-1997;

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New isolated polymerates that and encoded polypeptides, useful in adapostics, forensics, game mapping, identification of mutations esponsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3531 BP; 952 A; 901 C; 960 G; 718 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                     Claim 1; SEQ ID No 22567; 103pp; English.
                        Tang YT;
                        Drmanac RT, Liu C,
                                                  WPI; 2001-639362/73
(HYSE-) HYSEO INC.
                                                                P-PSDB; ABG22576
```

Expressed sequence tag; secreted protein; haematopoiseis regulator; tissue growth; activit; inhibhi; tumour invasion suppressor; EST; human; obsencerais chemoritesis; haemotasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.

New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, foetal lung, placenta, restes, brain, ovary, pitutary, retina and oolon cDRA libraries

Claim 1; Page 383-384; 633pp; English.

Local Similarity 100. nes 391; Conservative

Best Loca Matches

430

à g à g 셤 g à 용 à 유

550

à ₽ RESULT

à

Query Match

Lavallie ER, McCoy JM, Merberg Treacy M;

J, Jacobs K, Spaulding V,

Agostino MJ, Racie LA, WPI; 1999-070076/06.

98WO-US06954.

LS-OCT-1998.

(GEMY) GENETICS INST INC.

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The sequence represents an expressed sequence tagg (SST), and is a polymorphic contact of the invention may be a polymorphic contact of the invention may be a more than the invention of the sequence and protein encoded by them are perfected to have useful brighted acceptance and protein encoded by them say perfected to these useful brighted acceptance and protein encoded by them say perfected to treating preventing sequences and protein encoded by them say and the say of the sequence are also seared to be useful for gone of the sequence of the sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 AAGGACCIGCAGGACGIGICCAICACIGIGCICAACGICACICIGAACGACICIGGCCIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.7%; Score 324; DB 20; Length 471; 100.0%; Pred. No. 2.8e-147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; Pred. Mc.
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Matches 324; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 AACCCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGGAGGAGGTGGAGGCCACCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGTGGAATGGTTÖRACAGGCCCGAGGGCGGTAAAGATTTCCTTAATTTACGAGTATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    610 AATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCTGTGTGTGTGGAAGTGCCCTCGGAGACGGAGGCCGTGCAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 391; DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3319 CGCTGATCCCCTAAGAGTCACCGAGGAGG 3349
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Note: The sequence data for this parent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
TACACCTGCAATGTGTCCCGGGGAGTTTGAGGTTTGAGGCGCCATCGGCCCTTTGTGAAGACG
                                                   379 TACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGGGCGTTCGGCCCTTTGTGAGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement; medical imaging, diagnostic, genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 621 BP; 156 A; 155 C; 175 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel human diagnostic protein #22566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scification, but was obtained in electroni ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 22566; 103pp; English.
                                                                                                                                                               787 ACGCGGCTGATCCCCCTAAGAGTC 810
                                                                                                                                                                                                                               439 ACGCGCTGATCCCCCTAAGAGTC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAS86762 standard; cDNA; 621 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73
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                                                                                                                                                                                                                                           Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
                                                                                                                                            TGGAATGGCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAAC
                                                                                                                                                                      595 ATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCCCTGCAG
                                                                                                       58 ATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGGCCCCTTTCAGGGGCCCCTGCAG
                                                                                                                                                                                                                 715 GACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTTGAGGCGCATCGGCCC
                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human reproductive system related antigen DNA SEQ ID NO: 7659
                                     Indels
                                                                                                                                                                                                                                                                                         775 TTTGTGAAGACGACGCGGCTGATCCCCCTAAGAGTCAC 812
                                                                                                                                                                                                                                                                                                                        TTTGTGAAGACGACGGGGGGGATCCCCCTAAGAGTCAC 275
                 Pred. No. 1e-95;
; Mismatches 0;
100.0%; Fre-
                                                                                                                                                                                                                                                                                                                                                                                                                    AAL04971 standard; DNA; 4625 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
              Best Local Similarity 100.
Matches 218; Conservative
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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22-AUG-2000;

17.3%; Score 218; DB 23; Length 621;

Query Match

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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(without alignments) 426.578 Million cell updates/sec December 5, 2003, 17:55:23 ; Search time 80 Seconds OM protein - protein search, using sw model Run on:

1 MPAFNRLFPLASLVLIYMVS.....SDYLAIPSENKENSAVPVEE 215 US-09-936-680-2 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameters: 1107863 segs, 158726573 residues Searched:

1107863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Databa

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score		* Query Match Length DB	DB	QI	Description
-	1124			2	AAB36002	Human beta3 subuni
6	1124	100.0		55	AAB85206	Human novel sodium
m	1124	100.0		23	ABB05689	Human signal trans
4	1105	98.3	215	21	AAB36001	Rat beta3 subunit.
S	1105	98.3		55	AAB50243	Rat sodium channel
9	1024	91.1		22	AAM79212	Human protein SEO
7	986	87.7		55	AAB50245	Rat sodium channel
œ	942.5	83.9		22	ABG22517	Novel human diagno
6	843	75.0		21	AAB36020	Human beta3 subuni

Rat beta3 subunit	Novel human diagno	Rabbit sodium chan	Rat betal subunit,	Rat sodium channel		Novel human diagno	Human betalA sodiu	Rat sodium channel	Sodium channel bet	Human voltage-gate	Human protein SEQ	Human beta3 subuni	Rat beta3 subunit	Human beta3 subuni	Human myelin prote	Rat beta3 subunit	Human PRO7425 prot	Human transport pr	Human PRO protein,	Human PRO7425 prot	Human myelin-like	Mouse major periph	Human channel-rela	Human PRO1192 prot	Membrane-bound pro			Human angiogenesis			Human PRO polypept	secreted	-		Human secreted/tra
AAB36021	ABG22576	AAB50260	AAB36031	AAB62326	ABB82771	ABG22575	AAE18634	AAB62320	AAB20371	ABB11698	AAM80196	AAB36015	AAB36016	AAB36029	AAM52696	AAB36034	AAY72879	AAB60121	AAU83710	ABG74763	ABG79170	AAW94567	AAY41673	AAB33448	AAY66752	AAU12415	AAB65275	ABB95515	ABB84909	AAU83675	ABU66813	ABU67089	ABUS9894	ABU59168	ABU59315
21	22	22	21	22	24	22	23	22	55	22	22	21	21	21	53	21	22	22	23	24	23	18	50	21	21	22	22	23	53	23	24	54	54	24	24
159	1176	218	218	218	218	206	268	272	272	74	74	33	39	34	258	34	235	235	235	235	246	248	215	215	215	215	215	215	215	215	215	215	215	215	215
74.0	61.7	42.4	42.0	42.0	41,9	36.3	23.0	21.9	21.9	20.8	20.8	18.4	17.4	14.7	14.5	14.3	14.3	14.3	14.3	14.3	14.3	13.3	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1
833	694	477	472	472	471	408.5	258.5	246	246	234	234	207	196	165	163.5	161	160.5	160.5	160.5	160.5	160.5	149	147	147	147	147	147	147	. 147	147	147	147	147	147	147
10	11	13	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	58	58	30	31	35	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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AAB36002 standard; protein; 215 AA.
                                                                                            15-FEB-2001 (first entry)
                                                                                                                                 Human beta3 subunit.
                                                       AAB36002;
AAB36002
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Human; beta sub-unit; beta; andagest; anticonvulsatari; coerebcoprorective; vacorcopic; cardiant; nootropic; cytoottetic; dermaclogical; gan therapy; voltage-ted goodium channel; pain; dermaclogical; gane therapy; voltage-ted goodium channel; pain; geniteps; stroke; isothemnia; heart disease; Jacobsen Syndrome; familial nonthoreaffiti paraganglioma; phenylketonurka; Ganden Gharoot Warie Tooch disease.

Homo sapiens.

WO200063367-A1.

24-FEB-2000; 2000MO-EP01783. 26-OCT-2000.

15-APR-1999; 99US-0129473.

(WARN) WARNER LAMBERT CO. (UYCA-) UNIV CAMBRIDGS TECH SERVICES LTD.

Dixon A, Jackson A, Morgan K;

Cox P,

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                                                                                                                                                                                                                                                                                     The invention provides a novel heart-like sub-mit for voltage-gated codium in conclaiming holygeptide, specifically a sensory neurone specific channel (SNS) subunit. The novel beat-like subunit is useful for producing a cherapeutic agent which is useful treating pain in a patient. The subunit can be expressed by standard reconstants methodology. The presents a quanto a person of the man movel sodium channel betal-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMPYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPAFNRLFPLASLVLIYMVSVCFPVCVEVPSETAAVQGNPMKLRCISCMKREEVEATTVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPAFNRLFPLASLVLIYWVSVCFPVCVEVPSBTEAVQGNPMKLRCISCMKREEVEATTVV 60
                                                                                                                                                                         Novel sub-unit for voltage-gated sodium channel proteins for producing agents useful for treating pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 1124; DB 22; Length 215;
; Pred. No. 1.4e-97;
0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human signal transduction protein clone amy2_2f18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YRKVSKAEEAAQENASDYLAIPSENKENSAVPVEE 215
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                                                                Sanseau P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB05689 standard; Protein; 215 AA.
                                                                                                                                                                                                                                                 Claim 1; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 215; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                     (GLAX ) GLAXO GROUP LTD.
                                                                Powell AJ,
                                                                                                               WPI; 2001-398129/42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-055860/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AA;
                                                                                                                                     N-PSDB, AAF84146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200198454-A2.
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                                                                Plumpton M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 EWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC 120
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                                                                                                                                                                                                                 The present exquence is given in the claims of a specification relatings to a novel family of beta sub-unit procedure from a voltage-gared sociam channel, Haman and rate heat sub-units, which have been collectively identified as betal. have been isolated.

The polymuclocuties and polypepticides are used full for screening for agonists and antagonists of sociam channels. The agonists, attagonists, proceins and natagonists of sociam voltage-gated sociam of the state of the special control of the specia
                                                             Novel Impelia acide ende encoding a bereal submuist from a voltage-gated social chainel, and their corresponding polypeptides, useful for addecting and treating sodium channel associated conditions, e.g. pain, pleaps and stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPAFNRLFPLASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1124; DB 21; Length 215; 100.0%; Pred. No. 1.4e-97; cive 0; Mismatches 0; Indels 0;
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157..176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      duman novel sodium channel betal-like subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "transmembrane domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB85206 standard; Protein; 215 AA
                                                                                                                                                                                Claim 34; Fig 4; 88pp; English.
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Matches 215; Conservative
WPI; 2000-665241/64.
N-PSDB; AAC67837.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease.
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Domain
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NVSREFEREAHRPFVKTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTLMLLIEMIYC 180
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                                                                                                                                                                                                                            The present esquence is given in the claims of a specification relating to a novel family of beta sub-unit proceins from a voltage-gated sodium channel, Human and rat beta sub-units, which have been collectively identified as beta) have been isolated. The polymelostices and optopepticated are useful for screening for agonistic and anteologists of oddium channels. The agonistic, antegonists or conditions associated with voltage-gated sodium channels. Greating diseases or conditions associated with voltage-gated sodium channels, e.g. pain, wonchronwaftin paragnajionae, phenylercome, inchannels, henylercome, inchannels, henylercome, inchannels, and Charlow inchannels.
                                                                    Novel nucleic acids encozing a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for desecting and treating sodium channel-associated conditions, e.g. pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1105; DB 21;
Pred, No. 8.4e-96;
O; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AABS0243 standard; Protein; 215
                                                                                                                                                                                 Claim 33, Fig 4; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.3%;
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VPI; 2000-665241/64.
                                                                                                                                            epilepsy and stroke
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 AA;
                         N-PSDB; AAC67836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease.
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                                                                                                                                                The present involtion describes seasonlages and computer readable media comprising novel human cDNA sequences and clones destruct forest living the forest livering forest livering the control part of the present invention which encode the proteins given in ABBOGSE to the ABBOGSE. The human CDNA sequences and clones can be used in sequences the retrained by the used in a variety of applications, for example they may be used in a variety of applications, for change they may be used in prefit as a variety of applications, for change they may be used in prefit as a variety of applications, for change they may be used in prefit as a variety of applications, for change they may be used in prefit ling assays, for providing large arrays of human genetic meterial for implementing large-scale screening exartegies and for treating diseases via gone therapy procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMFYRPEGGKDFLIYEYRNGHQEVESPRQGRLQMNGSKDLQDVSITVLNVTLNDSGLYTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVSREFEFERAHRPFVKTTRLIPLRVTBEAGEDFTSVVSEIMMYILLVFLTLWLLIEMIYC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NVSREFEFEAHRPFVKTTRLIPLRVTBEAGBDFTSVVSEIDMYILLVFLTLWLLIEMIYC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Net, bets sub-unit; betals, analgeas; anticonvaluant, cerebroprotectives, vasotropic, cardiant, noortopic, cytostatic, dermacological, aggene therepy, voltage-quada sodium channal, pain, epilapsy, stroke, ischnamia, neart disease, ideoben Syndrome,
                  Human cDNA sequences and clones derived from human fetal brain, fetal kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPAFNRLFPLASLVLIYMVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVBATTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 1124; DB 23; Length 215; 100.0%; Pred. No. 1.4e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  familial nonchromaffin paraganglioma; phenylketonuria;
Charcot Marie Tooth disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YRKVSKAEEAAQENASDYLAIPSENKENSAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRKVSKAEEAAQENASDYLAIPSENKENSAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (WARN ) WARNER LAMBERT CO.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB36001 standard; protein; 215 AA
                                                                                                            Claim 1, Page 176; 611pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jackson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2000; 2000WO-EP01783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 215; Conservative
                                                                 screening and therapy
                                                                                                                                                                                                                                                                                                                                                                                                             215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat beta3 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dixon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200063367-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .5-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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EMFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWWGSKDLQDVSITVLNVTLNDSGLYTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 EWFYRPEGGKDFLIYEYRNGHQEVESPPGGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NVSREFERENHRPFVKTTRLIPLRVTBEAGEDFTSVVSBINMYILLVFLYLWLLIEMIYC 180
                                                                                                                                                                                                                                                            The invention relates to polymocleotides (AMX185-AMX183) and the cenceded polygeptides (AMY1832)-AMM1801031 that eachibit activity elating copyokine, cell proliferation or cell differentiation or which may induce production of other optokines in other cell populations. The polymocleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various syrokine-like activities, est one cell growth factor activity, haemstopoists regulating activity, itsue growth factor activity, haemstopoists argulating activity, itsue growth factor activity, immunomodulatory activity and activity, itsue activity and may be useful in the disponsis and/or frequency. I sukasmia, nervous system disorders, atthirtis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modes Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPAFNRLFPLASLVLIYMVSVCPPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; muscle contraction.
                            Cao Y,
ng ZW;
                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 195;
                     Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Ca
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang :
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat sodium channel beta3 protein Alrxa94h5 mature protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query March
91.1%; Score 1024; DB 22;
Best Local Similarity 100.0%; Pred. No. 3e-88;
Marches 195; Conservative 0; Mismarches 0;
                                                                                                                                                                                                                       Claim 20; Page 4260; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB50245 standard; Protein; 191 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YRKVSKAEBAAQENA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-2000; 2000WO-US13144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001 (first entry)
                                                                                                   WPI: 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 AA;
                                                                                                                            N-PSDB; AAK52345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-NOV-2000
                        Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
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                                                              Xue AJ,
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                                                                                                                                                  The present invention provides the protein and coding sequences of the rat sodium channel betal procein, designated Airava946. This protein is involved in the generation of pain and other sensory or perceptive nerve inpulses, in the sexablishment and endurance of mod, mentodegenerative and sides placeders, and in the control of muscle contraction, including movements such as the heartbark, delgestion and vascular cone. The sequences can be used in predictive medicine, screening and diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vacchin; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                               New rat sodium channel beta-3 subunit gene isolated from a rat dorsal 
toot ganglion CDAN library for use in chromoseme mapping, forensic 
medicine, monitoring clinical trials and therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MPAFURLFPLASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVBATTVV
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                                                                                                                                                                                                                                                                                                                                                                                Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                         98.3%; Score 1105; DB 22;
98.1%; Pred. No. 8.4e-96;
ive 0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM79212 standard, Protein, 195 AA.
                                                                                                                                                                                                                                                                                               assays, and in pharmacogenomics.
                                                                                                                Claim 9; Fig 2; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human protein SEQ ID NO 1874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0560875.
2000US-0598075.
2000US-0620325.
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20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001; 2001WO-US04098.
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                                                                                                                                                                                                                                                                                                                                                                                                                  fatches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                       215 AA;
N-PSDB; AAC90600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157190-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
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99US-0134198

14-MAY-1999;

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The invention relates to isolated polymuchocide (I) and conjugation relates to isolate polymuchocide (I) and conjugation relates to isolate by the product disease that restrict (RI) is insection (RI) primers of ligorates and for chromosome only disease and such control and the recombinant production of (III). The chromosome of the charitage of the sale owed in diagnostics as expressed sequence tags for identifying a polymers and insecting antibodies against it, detecting or control articly of (III) or to test disease states involving a confinitely a polyped in trissue, as an obscular testing many testing a polyped in trissue, as an obscular testing many testing and the binding partners are useful in medical angular products involving and testing became (III) or to the confinite and polymuchecide sequences have applications in the polypepic and polymuchecide sequences have applications in the polymorphic or genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and the produce dependent of sequences has and to produce other types of the same of the inventor.

Consideration of sequences of the invention.

Consideration of the sequence of the invention of the printed of the produce of the consideration of the printed of the produce of the inventor of the produce of the inventor of the printed of the produce of the inventor of the printed of the produce of the inventor of the printed of the printed of the printed of the produce of the inventor of the printed of the format discorder of the printed of the first expense.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 CNVSREFEREARRPFVKTTRLIPLRVTEBAGEDFTSVVSEIMMYILLVFLTLMLLIEMIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPAFNRLFPLASLVLIYWVSVCFPVCVEVPSETEA-VQGNPMKLRCISCMKREEVEATTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VEWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                        New isolated polymucleotide and encoded polypeptides, useful in adamostics, foremsics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerabtoprotective, wasorropic, cardiant; noorropic; cytostatic; gerantopic; cytostatic; gerantopic; cytostatic; spin; sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 22; Length 369;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 942.5; DB ....
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; SEQ ID No 52936; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human beta3 subunit peptide, SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 CYRKVSKAEBAAQENA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 CYRQVSKAEEAAQENA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.9%;
93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 93.99
Matches 184; Conservative
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                                                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 AA;
                                                                                                                                                                                                     N-PSDB; AAS86764
                                                                                                                                                                                                                                                                                                                                        biodiversity
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us-09-936-680-2.rag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTCNVSREFEFEAHRPFVKTTRLIPLR 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rett dodium hannel berås jrocesin, designared Airzapash; Airis protesin is impolsed in the generation of pain and other sensory or perceptive nerve impolses, in the establishment and endurance of mod, netrodegenerative and sleep dissorders, and in the control of muscle contraction, including movements such as the heartbeart, delgestion and vasculat correction, including equuences, can be used in predictive medicine, sorceming and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of the
                                                                                                                                                                                                                                                                                                                                                    New rat sodium channel beta-3 subunit gene isolated from a rat doraal root ganglion cDNA library for use in chromosome mapping, forensic medicine, monitoring clinical trials and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVVEWFYRPEGGKDFLIYEYRNGHQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTCNVSREFEFBAHRPFVKTTRLIPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 VTEEAGEDFTSVVSEIMMYILLVFLTIMLLIEMIYCYRKVSKAEEAAQENASDYLAIPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTEEAGEDFTSVVSEIMMYILLVFLTLMLFIEMIYCYRKVSKAEEAAQENASDYLAIPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 VCVEVPSETBAVQGNPMKLRCISCMKREBVEATTVVEWFYRPEGGKDFLIYEYRNGHQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 986; DB 22; Length 191;
Pred. No. 1.1e-84;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #22568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG22577 standard, Protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              assays, and in pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Fig 2; 145pp; English
                                                                                                                                                                    (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.78;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tang YT;
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23-AUG-2000; 2000US-0649167.
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Best Local Similarity 99.09
Marches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                         WPI; 2001-122743/13.
N-PSDB; AAC90600.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                      Curtis RAJ;
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119

(WARN) WARNER LAMBERT CO. (UYCA-) UNIV CAMBRIDGE TECH SERVICES LID.

99US-0129473

15-APR-1999;

24-FEB-2000; 2000WO-EP01783

40200063367-A1. Homo sapiens.

26-OCT-2000

Morgan K;

Dixon A, Jackson A,

Cox P,

MPI; 2000-665241/64.

Claim 36; Page 76; 88pp; English.

epilepsy and stroke -

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61 EWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acide encoding a beta-3 subunit from a voltage-gated acidim channel, and their corresponding polypepizides, useful for detecting and treating southum channel associated conditions, e.g. pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPAFNRLFPLASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVV
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                 UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                 Dixon A, Jackson A, Morgan K;
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                                                                                                                                                        24-FEB-2000; 2000WO-EP01783
                                                                                                                                                                                                                                                                              (WARN ) WARNER LAMBERT CO. (UYCA-) UNIV CAMBRIDGE TEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy and stroke -
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI, 2000-665241/64.
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Best Local Similarity
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                                                                                        26-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                            Cox P,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence as given in the claims of a specification relating to a novel family of hets mub-nic process, and which wollsage-gated sedium channel, Human and tab hearshe traw which have been collectively identified as heats, have been isolated the host processes of the polymetication and properties are useful for expensing for agonists and antagonists of sodium channels. The agonists antagonists of colium channels. The agonists antagonists or conflictions associated with voltage-gated sodium channels, or grantly expension of treating diseases or conflictions associated with voltage-gated sodium channels, e.g. path wonthan after receive isothermal, a hear (disease, coobsen syndrome, Panilla) wonthandfilm paragarglicam, phenylectomiza and Charcom Marie Tooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                when muster a condense and the management of the manage and a content of and their or corresponding polypoptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPARNALPPLASLULYWVSVCPPVCVEVPSETBAVQGNPMKLRCISCMKREEVBATTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MPAFNRLFPLASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NVSREFEFEAHRPFVKTTRLIPLRVTEEAGEDFTSVVSE 159
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75.0%; Score 843; DB 21; 100.0%; Pred. No. 2.4e-71; ive 0; Mismatches 0;

Matches 159; Conservative

à 셤 à g à 윱

Local Similarity 159 AA;

Seguence

disease. Query Match ö

Gaps ö 09

9

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Rat, Date aub-unit, betal, analgest; praniconvolasci; oproettic; derebcoprotective; varotropic; carciant, nootropic; cyrottetic; dermaclogico; pren Cherapy, voltoge-ated sedium channel; pain; sellepsy, stroke; sechaemia; heart disease; Jacobeen Syndrome; femilial nonthroadfilm partagnglioma; phenylketomuria; Gyndrome; Offancor Marie Tooch disease.
                                                                                      Rat beta3 subunit peptide, SEQ ID NO: 23.
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Rattus sp

AAB36021 standard, protein, 159 AA.

AAB3602

(first entry)

15-FEB-2001

AAB36021:

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124 REFBFBAHRPFVXTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTLWLLISMIYCYRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 RLLSFENYEHNTSVVKKIHLEVVDKANRDMASIVSEIMMYVLIVVIJIWLVAEMVYCYKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70 KDFL-IYEYRNGHQBVESP--FQGRLQWNGS---KDLQDVSITVLNVTLNDSGLYTCNVS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65 EBFVKILRYENEVLQLEEDERPEGRVVWNGSRGTKDLQDLSIFIINVTYNHSGDYQCHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the procein and coding expenses of the true Rediam channel being procein, designated Altroship. This protein is involved in the generator of pain and other sensory or perceptive nerve impulses. At the establishment and endurance of mood, neurodeseneative and altespoins codercers, and in the control of muscle contraction, including movements such as the heartbest, dispection and vascular totion. The esquence can be used in predictive medicine, acreening and dispnostic assays, and in pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 LAFVVGAALVSSAWGGCVEVDSETEAVYGMTFKILCISCKRRSETTAETFTEWTFRQKGT 64
                                                                                                                                                                                                                                                                                                                                          New rat sectium channel beta-1 subunit gene isolated from a rat dorsal
root gagglion cuba library for use in biromosome mapping, forensic
medicine, monitoring clinical trials and therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 LASLVLIYWYSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREBVEATTVVEWFYRPEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat, Pete sub-unit, beta3; analgesic, anticonvolascit; cerebroprotective; vasortopic; cardiant; nootropic; cytosetatic; demaclogical; gene therapy; voltage-geted sodium channel; pain; esplieps; stroke; sichsemia; heart disease; Jacobsen Syndrome; familia nonchromaffin paragonjaloma; phenylketonurta; donore; Mario Pooch disease; beta1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.4%; Score 477; DB 22; Length 2; Best Local Smilarity 49.5%; Pred. No. 9e-37; Indels Matches 106; Conservative 32; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 VSKA-EBAAQENASDYLAIPSENKEN-SAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 IAAATEAAQENASEYLAITSESKENCTGVQVAE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB36031 standard; protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 3, 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat betal subunit, SEQ ID NO: 44.
                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                          12-MAY-2000; 2000WO-US13144.
                                                                                                                                                                      99US-0134198,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IS-FEB-2001 (first entry)
Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                     WPI; 2001-122743/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 AA;
                                        WO200069912-A1.
                                                                                                                                                                      14-MAY-1999;
                                                                                     23-NOV-2000
                                                                                                                                                                                                                                                            Curtis RAJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB36031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                       쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                용
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                                                                                                                                                                                                                                                                                                                                                                                                                        The proposition [11] stration (ECT) primars, oligomers, and for thronosome polymerase chair restrictor (ECT) primars, oligomers, and for chronosome polymerase chair restrictor (ECT) primars, oligomers, and for chronosome polymerase chair and in recombinant production of [11]. The chair and in recombinant production of [11], the polymerides are also used in disposition as expressed sequence tags for reservoir normal activity of [11] or to treat disease states involving to creators normal activity of [11] or to treat disease states involving to (11) [11] is useful in gene thereby techniques to creators normal activity of [11] or to treat disease states involving to (11) [11] is useful in gene thereby techniques to creators for a complete and a second chair of the complete and an expension of a cities and production and partners are useful in medical segundar of cities and polymerical segundares have applications of metations of the products dependent on DNA and and and to produce other types of date and products dependent on DNA and disposition of minerical segundares. Absolute before traits to assess bicdiversity and classification of adaption of the invention.

Complete the sequence date for this parent did not appear in the printed specification, but, was optained in secretarion format directly from Wileo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       987 VSVCFPVCVEVPSETBAVQGNPMKLRCISCMKREEVBATTVVEMPYRPEGGKDFLIYEYR 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1047 NGHOBVESPPOGRLOMNGSKOLODVSITVANVILNDSGLYICKVSREPBFEARRPYVKIT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 NGHQEVESPFQGRLQWNGSKDLQDVSITVLAVTLANDSGLYTCNVSREFEFEAHRPFVKTT 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 VSVCFPVCVBVPSBTEAVQGNPMKLRCISCMKREBVEATTVVBWFYRPEGGKDFLIYEYR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat; sodium channel betal protein; Alrxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; muscle contraction.
                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, useful in diagnostics. Foresitor, spen mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61.7%; Score 694; DB 22;
100.0%; Pred. No. 2.9e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 52935; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rabbit sodium channel betal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AABS0260 standard, Protein; 218 AA.
                                                                                                                                                  Tang YT;
                                            31-MAR-2000; 2000US-0540217.
   30-MAR-2001; 2001WO-US08631
                                                                23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107 ŘLIPLRVÝŠE 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 RLIPLRVTEE 148
                                                                                                                                                                                           NPI; 2001-639362/73.
                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                             (HYSE-) HYSEO INC.
                                                                                                                                                                                                                      N-PSDB; AAS86763..
                                                                                                                                                                                                                                                                                                                                biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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8; Gaps

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The invention relates to a method of screening for a conditator of solium channel activity that computes contacting a candidate aboulator with a cell co-expressing a solium channel beeral a solumnint with a sodium channel atha submint, with a sodium channel atha solumnint with a sodium channel contact of the candidate modulator on the sodium channel function in the cell. The method is useful for identifying sodium channel activity modulators, preferably causing decreased beet a submit the expression. The modulators can be used to decrease neuropathic pain, and to decrease the number of febrile seitures in an individual. The present sequence expressions at the beautification is a beautification of the second correction and activities which the beautification is a submit, used in homology studies with the beautif submit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 KDFL-IYEYRNOHQEVESP--PQSRLOMNGS---KDLQDVSITVLAVVTLNDSGLYTCNVS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 EEFVKILAYENBVLQLEEDERFEGRVVWNGSRGTXDLQDLSIFITWVTYNHSGDYECHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 REFERENTED VKTTRLIPLRVTERAGEDFTSVVSEINNYILLVFLTLWLLIEMIYCYRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soreening for sodium channel activity modulators, used to decrease encopathic pain, comparises contacting a candidate compound with a cell expressing the channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LASLVLIYWVSVCFPVCVBVPSETRAVOGNPMKLRCISCMKREBVEATTVVBWFYRPEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LALVVGAVLVSSAWGGCVEVDSETEAVXGMTFKILCISCKRRSETTAETFTEWTFRQKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sodium channel; mutation; epilepsy; anticonvulsant; mutant; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.0%; Score 472; DB 22; Length 218; 49.1%; Pred. No. 2.7e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruman voltage-gated sodium channel mutant beta-1 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 VSKA-EEAAQENASDYLAIPSENKEN-SAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 IAAATEAAAQENASEYLAITSESKENCTGVQVAE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB82771 standard; Protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                 Examples, Fig 1B, 124pp; English.
                                                                                                                                                 (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                  99US-0156837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2002; 2002WO-AU00581.
                                                   29-SEP-2000; 2000WO-US27034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-2003 (first entry)
                                                                                                                                                                                                Rogers KE;
                                                                                                                                                                                                                                                   WPI; 2001-281683/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCN1B; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40200290532-A1.
                                                                                                  30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                D'Andrea M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L4-NOV-2002
05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB82771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 BEFUKILRXENEVLQLEEDERFEGRVVWNGSRGTKDLQDLSIFITUVTYNHSGDYECHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 KDFL-IYEYRNGHQEVESP--FQGRLQWNGS---KDLQDVSITVLNVTLNDSGLYTCNVS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 REFERENTREFVKTTRLIPLRVIEEAGEDFTSVVSBIMMYILLVFLTLWLLIEMIYCYRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 RLLFFDNYEHNTSVVKKIHLEVVDKANRDMASIVSEIMMYVLIVVLTIMLVAEMVYCYKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVVEWFYRPEGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LALVVGAVLVSSAWGGCVEVDSETEAVYGWTFKILCISCKRRSETTAETFTEWTFRQKGT 64
                                                                                                                                                                                                                                                                                                                                                                                 sodium channel, and their corresponding polypeptides, useful per a perception of the perception and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is given in a specification relating to a more latently of beets sub-unit proceins from a voltage-gated sodium channel. Human and rate bets sub-units, which have been collectively identified as the sai, have been isolated. The polymucleotides and polymptides are useful for escreening for agonists and antagonists of sodium channels. Hagonists, antagonists, proceins and moleic acids may be used diagnosing of treating diseases or conditions associated with that diseases, Jacobes Synthes, Panilial Insuring Contract, Statement and Charcot Maria Tricke, isochamia, what disease, Jacobes Synthes, Panilial Roberton Roberto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium channel; modulator; sodium channel beta-1A subunit; pain; rat; sodium channel beta-1 subunit; analgesic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Gaps
                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding a beta-3 subunit from a voltage-gated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.0%; Score 472; DB 21; Length 218;
49.1%; Pred. No. 2.7e-36;
tive 33; Mismatches 68; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat sodium channel beta-1 subunit amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 VSKA-EEAAQENASDYLAIPSENKEN-SAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 IAAATEAAAQENASEYLAITSESKENCTGVQVAE 218
                                                                                                                                                                                                (WARN ) WARNER LAMBERT CO.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                       Cox P, Dixon A, Jackson A, Morgan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB62326 standard; Protein; 218 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 88pp; English.
                                                                                                  24-FEB-2000; 2000WO-EP01783
                                                                                                                                                 99US-0129473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                          WPI; 2000-665241/64.
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       WO200063367-A1.
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                                                                                                                                                     15-APR-1999;
                                                   26-0CT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aatches
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8, Caps

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

December 5, 2003, 22:59:23 ; Search time 44 Seconds (without algements) 469:215 Million cell updates/sec Run on:

1 MPAFNRLFPLASLVLIYWVS......SDYLAIPSENKENSAVPVEE 215 US-09-936-680-2 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308

Total number of hits satisfying chosen parameters:

Minimum DB sed length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:* PIR 76:* Database :

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ole.				
Result		Query				
No.	Score	Match	Match Length DB	13	GI	Description
-	477	42.4	218	N	JC4788	
c	472	42.0	218	N	A42737	
m	471	41.9	218	C)	A55734	cha
4	175	15.6	248	н	MPRT0	myelin PO protein
S	163.5	14.5	248	~1	JH0252	
v	163.5	14.5	251	7	138053	pro
7	159	14.1	219	н	A29128	
8	154.5	13.7	247	٦	A54662	P0
ø	144.5	12.9	246	н	A32999	
10	140.5	12.5	249	-1	A61087	â
11	118	10.5	215	cı	A57843	sodium channel bet
13	117	10.4	186	ĸ	161783	sodium channel bet
13	111.5	9.6	820	~	S17295	fibroblast growth
14	111.5	6.6	821	г	TVMSBK	fibroblast growth
15	110.5	9.6	1462	Н	B36182	protein-tyrosine-p
16	109	9.1	800	7	TVHU2F	fibroblast growth
17	107	9.5	800	~	A48991	heparin-binding gr
18	107	9.5	801	01	155363	fibroblast growth
19	103.5	9.5	129	0	\$57884	T cell receptor WI
20	103.5	9.5	353	C)	S51242	heparin-binding fi
21	103.5	9.5	372	~	C39371	Ig V-region-like B
22	101.5	0.6	806	N	A35963	protein-tyrosine k
23	100.5	6.8	750	N	841051	fibroblast growth
24	99.5	-	131	7	B32513	Ig kappa chain pre
25	99.5	6.8	131	N	B30577	Iq kappa chain pre
26	99.8	6.8	131	N	PT0178	Ig kappa chain pre
27	99.5	6.8	823	~	TVHUF2	fibroblast growth
28	98.5	8.8	118	N	\$24539	Ig kappa chain V r
29	98.5	8.8	133	7	D34904	Ig kappa chain pre

fibroblast growth protein-tyrosine k	chair	Ig kappa chain pre T-cell receptor de	ig light chain pre fibroblast growth	keratinocyte growt fibroblast growth	protein-tyrosine k Ig kappa chain V r	Ig kappa chain V r Ig kappa chain V r	Ig kappa chain pre Ig kappa chain pre
S41050 B35963	JC4954 S24533	C29380 S36320	B39276 A54846	A38429 B54846	S24108 S24529	S24535 S24500	B34904 S09259
748 2 823 2	379 2	130 2	131 2	707 2	824 2 118 2	118 2	131 2
	8.8	8.8	8.5	8.8 6.5	8.8 2.4.	4.4	8.8
98.5	98.5	96 8	95.5	95.5	95.5	94.5	94.5
30	33	35	36	38	41	43	44 54 55

ALIGNMENTS

RESULT 1 JC4788	-				
sodium	channel	sodium channel protein betal chain - ra	beta1	chain	· ra
	Day . DA	C. Species. Orientalems amplemen (domes	2	1110	Domo

C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 10-May-1996 #Bequence_revision 16-Aug-1996 #text_change 05-Nov-1999 stic rabbit)

Cincession; JOS188

R.Belcher, B. M.; Howe, Jr.R.
Gene 170, 285-286, 1996 and N. encoding the sodium channel betal subunit from rabbit. AlRetence number: JOS1989, MUID:96233151; PMID:9665631

Airoclession: 1-204788
Airoclecule type; mRNN

A;Gene: obetal A;Gene: obetal Keywords: glycoprotein; membrane protein; muscle; transmembrane protein F;161-182;Moanin, transmembrane #status predicted <PMA> P;93,110,114,115/Binding site; carbohydrate (Asn) (covalent) #status predicted

10 LASLVLIYWVSVCPPVCVEVPSETEAVQGNPMKLRCISCMKREEVBATTVVEMFYRPEGG 69 5 LAFVVGAALVSSAWGGCVEVDSETEAVYGMTFKILCISCKRRSETTABTFTEWTFRQKGT 64 8; Gaps Length 218; Omery Match 42.4%; Score 477; DB 2; Length 218 Best Local Similarity 49.5%; Pred. No. 2.5e-35. Matches 106; Conservative 32; Mismatches 68; Indels

à 셤 ò 윱 à 셞 ò 용

RESULT 2

C.Species Rattus norvegicus (Norway rat) C.Date: 0-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999 C.Accession: AA270 sodium channel beta 1 subunit - rat

Rigom, L.L.; De Jongh, K.S.; Patton, D.B.; Reber, B.F.; Offord, J.; Charbonneau, H.; W Affice 265, Prisary structure and functional expression of the beta 1 subunit of the rat b Affice: Prisary structure and functional expression of the beta 1 subunit of the rat b

us-09-936-680-2.rpr

à 윰 ò 셤 ò

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Affictons: 32,17,18(3): 150/11, 195/2; 21,105/2)
Cjeuperfemily: myelin Porcetan ; memunoglobulin homology
Cjeuperfemily: myelin Porcetan; memanoglobulin homology
Fil-29/Domesin: signal engemene #fectus predicted <5105
Fil-29/Domesin: signal engemene #fectus predicted <5105
Fil-29/Domesin: signal procetan #fectus predicted <6105
Fil-515/Jomesin: extracellular #fectus predicted <6070>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K. Rilemke, G. A. Azel, R.
Cell 40, 501-508. 1981-888. 1982. Sequence of a CDNA encoding the major structural protein of per
A.Reference number number 1872822, WIID:85124601, PWID:2578885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nauron 1. 7; 18, 1988 ...
AiTitle: Leolation and analysis of the gene encoding peripheral myelin protein zero.
A:Reference number: 400622; Willo:90166482; PKID:2483091
A:Accession: 400622; Willo:90166482; PKID:2483091
A:Accession: 40762 DMA
A:Residues: 1. 248 - (Elfert
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                                                                                                                                                                                                                                                                              70 KDFL-IYEYRNGHQEVESP--FQGRLQWNGS---KDLQDVSITVLANTLNDSGLYTCNVS 123
                                                                                                                                                                                                                                                                                                                                        65 BEFVKILRYENBVLQ1EEDERFEGRVVWNGSRGTKDLQDLSIFITNVTYNHSGDYECHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 REFEFERAHREFVKTTRLIPLRVTEEAGEDFISVVSEINMYILLVFLTLMLLIBMIYCRK 183
125 RLLEFRHYBHYTSVVKKHHEVDSANROMASIVSEINMYVLIVVLTHAVARATCVFKK 184
125 RLLEFRHYBHYTSVVKKHHEVDSANROMASIVSEINMYVLIVVLTHAVARATCVFKK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 FEAHRPFVKTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTLWLLIEMI-YCYRKVSK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 -----IVGKTSOVTLYVFEKVPTRYGVVLGAVIGGILGVVLLLLLPYLIRYCWLRROA 188
                                                                                       10 LASLVLIYWVSVCFPVCVEVPSETBAVQGNPMKLRCISCMKREEVEATTVVEWFYRPEGG 69
                                                                                                                                                                        s LALVVGAALVSSACGGCVEVDSETEAVYGMTFKILCISCKRRSETNÄETFTEMTFRQKGT 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Rattus incregizus (Norway rat)
Crüste: 30-28p-1987 Hagquence_Ervision 30-Sep-1987 #text_change 18-Feb-1995
Kriemko, 6.7, imana; E.; Pattereon, J.
       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Gaps
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F.45-13/Domain: transmembrane Hetetus predicted <TMD>
F.180-240/Domain: transmembrane Hetetus predicted <TMD>
F.120-240/Domain: irransmembrane Hetetus predicted <TMD>
F.120-240/Dinding site: carbobyldrate (Amn) (covalent) #ethus predicted
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       69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 15; DB 1; Score 175; DB 1; Similarity 28:14; Pred. No. 1.4e-07; 59; Conservative 34; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 VSKA-BERAGENASDYLAIPSENKEN-SAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 IAAATETAAQENASEYLAITSESKENCTGVQVAE 218
       Matches 106; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 AEE---AAQENASDYLAIPSENKENSAVPV 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myelin PO protein precursor - rat
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A; Residues: 1-248 < LEM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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J. Biol. Chem. 269, 7271-579, 1394
A.R. Artiles Vollage-gated And Channel benefin and RNA expressed in adult human skelet
A.Reference number: ASA309, MOID:94171709, PWID:9125960
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A,Reference number: A55734; MUID:95154833; PMID:7851891
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R:NGC14cchey, A.J.; Cannon, S.C.; Slaugenbaupt, S.A.; Gusella, J.F.
Hum: Nol. 'Genet. 2, 745-749; 1993
M:Tritle: The Coloring and expression of a sodium channel beta 1-subunit cDNA from human i
A:Reference number: Islasi4; MUID:93367746; PMID:83367782
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FrliJyDomain: signal sequence Heidurg predicted <SIG»
FrliJyDomain: signal sequence Heidurg predicted <SIG»
Frijal, 120,20main: transmembram Heidurg predicted <TUTMys / P.59,110,113F/Ainding site: carbohydrate (Asm) (covalent) Heratus predicted
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                                                                                                                                                                                                                                  A./Cross.-references: GB:191809; NID:9210664; FIDN:AAA88513.1; PID:92106665
A.Ropesimental source: brain
A.Ropesimental source: brain
C.Koywords: transsembrane protein
C.Koywords: transsembrane protein
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                                                                                              A;Status: preliminary; not compared with conceptual translation A; Molecule type: nucleic acid; protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 42.0%; Score 472; DB 2; Length 21% Best Local Similarity 49.1%; Pred. No. 6.78-33; Matches 68; Indels Matches 105; Conservative 33; Mismatches 68; Indels
A;Reference number: A42737; MUID:92271207; PMID:1375395
A;Accession: A42737
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49.5%; Pred. No. 8.1e-33;
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A;Molecule type: MRNA
A;Molecule type: MRNA
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A,Cross-references: GDB:127281; OMIM:600235
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A,Residues: 1-218 <MAK1>
A,Cross-references: GB:U12189
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A; Residues: 1-218 < MAK2>
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Best Local Similarity
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CiAcession: 138053; A45441, 5431, 5431
CiAcession: 138053; A45441, 5431, 5431
R.Rautemacuse B., 1701, 1702, 1994
A. Riller in Chemitication of a denovinestional mutation in Po in a patient with a Dej Atacession: 138053; WIDD:95136435; PMID:95136405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Wolecule type: protein
Aseatues: 1-219 -82Kx
C;Superfamily: myelin Po protein; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein; myelin; phosphoprotein; Schwann cell; struc
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Cipectes Boo pringenius tarura (cattle)
Cipectes Boo pringenius tarura (cattle)
Cipectes Boo pringenius degenerace_revision 10-Sep-1999 #text_change 21-Jan-2000
Cipectesion A29128
Ristandan X. 1. Kitamara, K.; Yoshimura, K.; Nishijima, T.; Uyemura, K.
Bibl. Chem. 262, 4308-444, 1387
A. Title: Complete animo caid sequence of PO protein in bovine peripheral nerve myelin.
A. Reference number: A29128, MUID:87166035, PMID:2435734
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A.Moleule (Prg. DMB;
A.Moleule 1.251 (MB);
A.Coras-references: BMBL, Z12/18; NID.9469516; PIDN:CAA83513.1; PID:9469517
A.Coras-references: BMBL, Z1, Li, Lepercq, J.; Trofatter, J.A.; Ravetch, J. V.; Lebo, R.St., T. Scooke, D.G.; Li, A.; A. 90, 1834.9, 1935-10866, 1393
A.TILLE: Myell, profession gene mutated and Carcor-Marie-tooth type 1B patients.
A.Roference number: A49643; WID:94068501; PMID:7504284
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A; Note: sequence extracted from NCBI backbone (NCBIP:139777)
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A. COMER. CDB. CMT1B; CMT1B; CMT1A. CMT. CMT1B; CMT1A. CMT1B; CMT1A. CMT1B; CMT1A. CMT1B; CMT1B
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                                   ---RKVSKAEE 189
                                                                                                                                                                      189 ALORRISAMEK 199
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A; Residues: 50-105 <SU1>
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R.Phamerbah D. Receptal, Y.; Blanquet, F.; Mattei, M.G.; Roeckel, N.; Latour, P.; Chaze M. P. S. 2003--0364, 1991 merchan sero genes structure and localization in th Artitle: The major peripheral myellin protein zero genes structure and localization in th ArAccession: 139378
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A.Residues: 1-63,64-115, RES.
A.Residues: 1-63
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A/Reference number: 158118; MUID:94035114; PMID:7693130
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A; Ederences (18 10) 0337; GB: D90501; NID: 9220073; PIDN: BAA01395.1; PID: 9220074
A; EHYQREAKE, X; OBnishi, A; TixAded G.; Pukunkima Y; Nurai, Y.
Bicochem Biophye. Res. Commun. 194, 1317-1322, 1993
A; TixLes Moretion of the myelin Po gene in charcot-marie-tooth neuropathy type 1.
A; Rockeston number 100704
A; Noclecule type: NRRA
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N;Alternate names: myelin protein zero
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C.Comment: This protein is found only in peripheral nervous system Schwann cells.
C.Comment: This protein is found only in peripheral nervous system Schwann cells.
C.Superfamily: mpelin Po protein; immunoglobulin homology
C.Kepyords allycoprotein; myslin; Schwann cell; structural protein; transmembrane protein;
P.1.29 Dommin: signal sequence #sterus predicted <816s.
P.1.29 Dommin: signal sequence #sterus predicted <816s.
P.1.29 Thomain: extraochlula; #sterus predicted <817s.
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AyReference number: A&1087; MUID:90204597; PMID:1690817
AyAccession: A&1087
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Ciskwords glycoprotein; membrane protein; wpelin; Schwann cell; structural protein
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                                                                                                                                                                                                                                                                                                                                                                                       16 IYMVSVCFPVCVBVPSETEAVQ------GNPMKLRCISCMKREEVEATTVVEMFYRP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LFCCSVLYAFSVLRPSQGISVSTHHNLHKTVGSDVTLYC-GFWSNEYVSDLTTLSWRFRP 68
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C.Species: Gallus gallus gallus (chiedon)
There: 10-691-1999 Hsequence_revision 10-8ep-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                       27; Gaps
                                                                                         A; Cross-references: GB:X16714; NID:g63976; PIDN: CAB37865.1; PID:g4467434
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F:154-129/Domain: immunoglobuliin homology (4Rp)
F:154-129/Domain: intransmembrane #status predicted (4RP)
F:120-249/Domain: intransmembrane #status predicted (4RP)
F:120-249/Domain: intransmembrane (4Rn) (covalent) #status experimental
                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 25.8%; Pred. No. 54-6-05.
Matches 49; Conservative 37; Mismatches 77; Indels 27;
Matches 49; Conservative 77; Mismatches 77; Indels 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 RQAVLQRRLSAMEKGKLQRSAKD 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurosci. Res. 25, 143-151, 1990
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48; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 YCYRKVSKAE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 YIVERRARSE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sest Local Similarity
                               A; Molecule type: mRNA
A; Residues: 1-246 <SAA>
A.Status: preliminary
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A.Accesson: A22999
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R.You, K.H.; Haish, C.L.; Hayes, C.; Stahl, N.; Francke, U.; Popko, B.
A.Title: DNA sequence, genomic organization, and chromosomal localization of the mouse.
A.Rocession: Assets R54662; WIID:91244320; PMID:1709914
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                                                                                                                                                                                                                                                                                                                                                                                            60 IDEVGIFKERIQWYGDPHRKDGSIVIHNLDYGDNĞIFİCDVKNPPD-----IVGKİSQV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 PLRVTEEAGEDFTSVVSEIMMYILLLVFLTLWLLIEMI-YCYRKVSKAEEA---AQENASD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 TLYVFEKVPTRYGVVLGAVLGGVLGVVLIALLIPYLIRYCWLRRQAALQRRLHAMBKGKL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 DFL-IYEYRNGHQEVE--SPFQGRLQMNGSKDLQDVSITVLNVTLNDSGLYTCNVSREFE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 DAISIFHYAKGQPYIDEVGAFKERIQWYGDPRWKDGSIVIHNLDYSDNGTFTCDVKNPPD 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 FEAHRPFVKTTRLIPLRVTBEAGEDFTSVVSEIMMYILLUFLISMI-YCYRKVSK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 -----INGKISQVILYVPEKVPTRYGVVLGAVIGGILGVVLLLLLFYLIRYCWIRRQA 187
                                                                                                                                                                                                                                                                                                                             94 VE--SPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTCNVSREFERHRPFVKTTRLI 141
                                                                                                                                                                                                   25 VCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVVEWFYRPEGGKDFL-IYEYRNGHQE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ASLVLIYWVSVCFPVCVEVPSETEAVQGNPMXLRCISCMKREEVEATTVVEWFYRPEGGK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 SSLVL----SPALAIVVYIDRRIYGAVGSQVTLHC-SFWSSEWVSDDISFTWRYQ-EGGR 73
                                                                                                                                                                                                                                                                   1 IVVYTDKEVHGAVGSQVTLYC-SFWSSEWVSDDLSFTWRYQPEGGRDAISIFHYAKGQPY 59
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CiSpecies: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
CiAccession A22999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         myelin PO protetin - mouse
C.Species: Mus mussculin (house mouse)
C.Jbate: 10-5ep-1399 #sequence_revision 10-8ep-1999 #text_change 21-Jan-2000
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                                                               14.1%; Score 159; DB 1; Length 219;
flarity 26.5%; Pred. No. 2.8e-06;
Conservative 31; Mismatches 99; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 247;
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13.7%; Score 154.5; DB 1; Length 2
Bert Local Similarity 27.6%; Pred. No. 7.6e-06;
Matches 58; Conservative 34; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Superfamily: myelin PO protein; immunoglobulin homology F;43-128/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 ALGRELSAMEKGRFHKSSKDSSKRGRGTPV 217
F;14-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 YLAIPSENKENSAVPV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 HKTAKDASKRGRQTPV 189
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A, Residues: 1-247 < YOU>
A, Cross-references: GB: M62427
                                                                    Query Match
Best Local Similarity
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Picholater growth factor receptor bek prequesor — mouse
M.Alternate names bek transforming pyotekin; fibroblast growth factor receptor 2; kerat,
Contains, protein-tyrasine kinase (BC 2,7,1,112) bek
C. Species manaculas (house mouse)
C. Date 30 - Mn 199 species contains the mouse)
C. Accesson A4442, A3137 Ba, P.; Moscatelli, D.; Kormbluth, S.; Hanafusa, H.; Basilico,
R.;Mansokhani, A.; Dall Ea, P.; Moscatelli, D.; Kormbluth, S.; Hanafusa, H.; Basilico,
A.; Title: Gharaccerisation of the marine Bsk (Ebroblast growth factor (RGP) receptor: ac
A.; Accession index: A44142, MUID:92228773; PMID:373495
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R;Nornbluth, S. r. Paulson, K. E.; Hanafusa, H.
Nol. Cell. Biol. 8, 541-5544, 1986
Nol. Cell. Biol. 1970sine kinse Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes Jenes
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AjRosatuces; 1-821 «MAN»
AjRosatuces; 1-821 «MAN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homology; prote
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; growth factor receptor
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109 GHGK----IYLQVLLEVPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRR-----KKE 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 EYTCLAGNSIGISFHSAWL-TVLPAPVREKEITASPDYL----ELAIYCIGVFLIACMVV 392
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A:Resides: 477-67-681 KORS
A:Crose-references1 GB:W23362; NID:g533219; PIDN:AAA37285.1; PID:g533220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 BMIYCYRKVSKABEAAQBNASDYLAIPSENKENSAVPV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 TVIFCRMKTTTKK-----PDFSSQPAVHKLTKRIPL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.12;
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                                                                                                                                                                                                                               192 QENASDYLAIPSENKENSAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 EVESPFQGRLQW-----NGSK----
                                                                                                                                                                                                                                                                                                                                                                            160 OKLSTDDLKTEEEGKTDGEGNAED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-820 <RAZ>
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                                         A; Gene: bek
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                                                                                                                                                                                                                                                       socium channel beta 2 subunit - rat
Species Ratus norvegicus (Norway rat)
Cipate: 02-Nul-1996 #egeqence_revision 02-Jul-1996 #text_change 05-Nov-1999
Cipate: 02-Nul-1996 #egeqence_revision 02-Jul-1996 #text_change 05-Nov-1999
Riscom, Lui. 857941
Riscom, Lui. 857941
Ajfile: 843-442, 1995
Ajfile: Strouter and Prnction of the Beta 2 Subunit of Brain Sodium Channels, a Transm
Ajfile: Strouter and Prnction of the Beta 2 Subunit of Brain Sodium Channels, a Transm
Ajfile: Strouter and Norvella Null 1996 February 17 Aprocession AST943
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A.Title 8, 373-442, 1995
A.Title 8, 373-442, 1995
A.Title 8, A.Title 8, A.Title 8, A.Title 19, A.Title 8, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title 19, A.Title
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 LKLER-FGDRVEFSGNPSKYDVSVTLKNVQLEDEGIYNCYITN--PPDRHRGHGK---1 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 PLRVTEBAGEDFTSVVSEIMMYILLVFLTLWLLIEMIY-CYRKVSKAEBAAQENASDYLA 200
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                  51 VLOFRMKIINLKLERFGDRVEFSGNPSKYDVSVTLKRVQLEDEGIYNCYIIN--PPDRHR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 PFVKTTRLIPLRVTEBAGEDFTSVVSEIMMYILLVFLTLWLLIEMIX-CYRKVSKAEEAA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Cross-references: EMBL: U37026; NID: 91086496; PIDN: AAC52967.1; PID: 91086497
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C.5pecies Rattus novegalcus (okvayo rat)
C.5peci 12-Apa-1196 Resquence_revision 11-Aug-1996 #text_change 05-Nov-1999
C.Dete: 12-Apa-1196 Resquence_revision 12-Aug-1996 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;MoLeoule type: mRNA
Residues: 1-215 <RES>
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Best Local Similarity 25.1%
Matches 49; Conservative
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Matches 49; Conserva
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A, Residues: 1-186 <RES>
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A; Introns: 50/3; 120/2
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63 FYRPEG-GKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVS----ITVLNVTLNDSG 116
                                                                                                                                                                                                                                                                                                                  117 LYTC-----NVSREPERBAHRPEVKTTRLIPLRVTEEAGEDFTSVVSBIMAYILL 166
                                                                                                                                                                                                                                                                                                                                                                                                        109 NYTCIAQIGQMHSIBFQVKPYLP-SKVLQSIPDRIKRKIKQD------VMLYCLI 156
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Proc. Hall Acad. Sci. U.S.A. 86, 8698-8702, 1999
A.Title: A Enaily of receptor-linked procedin tyrockine phosphateses in humans and Drosoph A;Reference number: Asisis, MUID:90046860; PWID:2554328
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                                                                                                                                                                                                                                                                                                                               procedin-tyrosine-phosphatase (EC 3.1.3.48), receptor type P7869D precursor - fruit fly NALexnerse names: procedin-tyrosine-phosphatase DPTP (S.89eriase names: procedinal andanogasce: C.89eriase names) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase) (S.89eriase
                        Fp.1-2.7/Domain. signal sequence Heature predicted <515.5
Fp.1-2.23/Peroduct: fibroblate growth feetor receptor bek Heatus predicted <4407>
Fp.17-2.33/Domain: immungajobulin homology <1100.
Fp.17-2.99/Domain: transmembrane Heature predicted <7000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 9.9%; Score 111.5; DB 1; Length 821; Beet.Locad Similarity 25.9%; Pred. No. 0.12; Indels 39; Gaps Matches 41; Conservative 33; Mismatches 55; Indels 39; Gaps
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No. 0.28; DB 1; Length 1462; 15milarity 26.7% pred. No. 0.28; Conservative 47; Conservative 31; Mismatches 61; Indels 37; Gaps
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11097/Active site: Cys (phosphocysteins intermediate) #strueture predicted
11103/Active site: cubencysteins intermediate; #struetured
11313/Active site: cubencysteinspec
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A.Residnes: 1.1462 - 278.
A.Cross-references: GB.M77699, NID:g158188, PIDN:AAA28842.1, PID:g158189
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

December 5, 2003, 20:51:34 ; Search time 26 Seconds (without alignments) 388.77 Million cell updates/sec

1124 1 MPAFNRLFFLASLVLIYWVS......SDYLAIPSENKENSAVPVEE 215 US-09-936-680-2 Perfect score: Sequence: Title:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched: Total number of hits satisfying chosen parameters:

127863

Minimum DB seg length: 0 Maximum DB seg length; 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES

Result No.	Score		Query Match Length DB	DB	аı	Description	:
-	4	٦,		٦	CIB3 HUMAN	Q9ny72 homo sapien	La La
71	477	42.4	218	ч	CIB1 RABIT	P53788 oryctolagus	gg
m	472	42.0	218	H	CIB1 RAT	Q00954 rattus norv	Š
4	471	41.9	218	-	CIB1 HUMAN	Q07699 homo sapien	en
Ŋ	468	41.6	218	н	CIB1_MOUSE	_	'n
9	175	15.6	248	М	MYPO RAT	P06907 rattus nor	ž
7	172	15.3	248	et	MYP0 MOUSE	P27573 mus musculu	'n
00	163.5	14.5	248	-	MYPO HUMAN	P25189 homo gapien	en
6	159	14.1	219	н	MYPO BOVIN	bog	8
70	149	13.3	215	٦	EVA1 MOUSE	O70255 mus musculu	1n
11	147	13.1	215	н	EVA1 HUMAN	O60487 homo gapier	en
12	144.5	12.9	246	ч			τn
13	140.5	12.5	249	-	MYPO CHICK	P37301 gallus gal	ī
74	118	10.5	215	Н	CIB2 RAT		Š
15	111.5	9.9	821	Н	FGR2 MOUSE	P21803 mus musculu	2
16	110.5		215	н	CIB2 HUMAN	7	en
11	110.5	9.6	1462	-1	PTP6_DROME		ø
18	101	9.5	801	+		Q61851 mus musculu	2
19	106	9.4	537	-	IR18_MOUSE		'n
20	101.5		908	н	CEK2_CHICK	gallu	7
2.1	99.5	6.8	821	ď		рошо	ea
55	66	8.8	541	~	IR18 HUMAN	homo	en
23	98.5	8.8	823	-	CBK3_CHICK	gallu	ננ
24	94.5	8.4	319	н	A33 HUMAN	homo	en
25	93.5	8.3	112	н	LV6B HUMAN	P01722 homo gapien	en
56	93.5		131	н	TVA1 HUMAN	homo	eu
5.	93	8.3	806	ч	FGR3 HUMAN	homo	en
28	92			~	PAS2 SCHAM	schis	rc
53	90	8.0		н	CXAR HUMAN	P78310 homo sapien	en
30	89			н			ae
31	88.5	7.9	365	н	CXAR_MOUSE	P97792 mus musculu	ր
35	87.5	7.8		M	CD7_MOUSE	0283 mus mu	크
33	86.5	7.7	224	-	UL01_HCMVA	P16719 human cytom	Ę

	P42159 geodia cydo P05537 homo sapien P01648 mus musculu		
JAMI BOVIN SHSI HUMAN BAST MOUSE	RTK2 GEOCY HB23 HUMAN KV50 MOUSE	CD83 HUMAN KV2F HUMAN HB2X HUMAN	BFR2_HUMAN PVR_HUMAN YYOI_CAEEL
44		аан	-
298	261	205 133 268	654 417 490
7.7	6.4.4	24.4	4.4.4.
86.5 85.5	84 84 85 85 84 85 84	83.5 83.5	83.5 83 83
35	2000	0 4 4	43 45 5

ALIGNMENTS

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Igom 1.1., De Josep K.S., Patton D.B., Raber B.F.X., Offord J., Charbonness H.W. Waith X., Colding A.L., Catterall W.A.,
Parlang structure and functional expression of the beta 1 subunit of the rat brain sodium channel.'

- FURCATION STRUCTURE AND THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL PROMODIANION CHOCLAIN THE BREAK OF THE SCOILDM CHANNEL THE BREAK OF THE SCOILDM CHANNEL THE BREAK STRUCTURE ALMAN SUBURIT FIGURATION OF THE HETRIGOTERMENT COMPLEX OF THE SCOILDM CHANNEL FOUNDERS FROM BRAIN, SEELETAL MUSICLE, AND HEAVE.
                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42.4%; Score 477; DB 1;
49.5%; Pred. No. 9.3e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 VSKA-BEAAQENASDYLAIPSENKEN-SAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-001-1993 (Rel. 26, Created)
01-001-1993 (Rel. 26, Last sequence update)
15-56P-2003 (Rel. 42, Last annotation update)
Sodium Channel beta-1 subunit precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GECNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
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                                                                                                                                                   EMBL; U35382; AAB17572.1; -.
                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                            160
182
218
150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 EWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EWFYRPEGGKDFLIYEYRNGHQEVESPFQGKLQMNGSKDLQDVSITVLNVTLNDSGLYTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NVSREFEFEAHRPFVKTTRLIPLRVTEBAGEDFTSVVSEIMMYILLVFLILWLLIEMIYC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NVSREFEBRAHRPVKTTRLIPLRVTBBAGBDPTSVVSBIMMYLLLVFJTLMLLIBMIXC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPAPNRLFPLASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPAFNRLPPLASLVLIYWVSVCEPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning of the cDNA encoding the sodium channel beta 1 subunit from
PERMY PRODUCT) igr. 1.
SMART; SMOG409; IGr. 1. I.
PROSTER; PSEG083; IC. CLIKE; 1. I.
PROSTER; PSEG083; IC. CLIKE; 1. I.
STORT CHARME!, PREMISHENCE; PODELIN COMPANIA.
SIGNACOPTOCKETH; SIGNAL; Immunosphobilin Compania.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Oryctolagus cuniculus (Rabbit).
Mammalia; Butheria; Jagomorpha; Laporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGOPONNS FROM BEALTH, SKELEPTAL MIGGLE, AND HEART,
-1- SUBUNIT: THE SODIUM CHANNEL CONSISTS OF A PORE-PORMING ALBERT ASSURINT, BETA-1 AND BETA-2 SUBUNITS. BETA-1 IS NONCOVALENTLY ASSULTATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . . .) (POTENTIAL)
70FGC604E9E26662 CRC64;
                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SURJEAR LOCATION: Type I membrane protein.
-- SURJEARTY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 1124; DB 1; Length 215; Pred. No. 8.3e-94; 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Sciatic nerve;
MEDLINE=96235151; PubMed=8666261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last amnotation update)
Sodium channel beta-1 subunit precursor.
                                                                                                                                                                                                                                              IG-LIKE C2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 AA
                                                                                                                                                                                                                                                           POTENTIAL.
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121 N
24702 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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215; Conservative
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215
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121 1
215 AA;
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PS3788;
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Matches 215
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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the Buropean Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this steement is now removed. Usage byt and for commercial entities requires allections expression (See http://www.isb-sib.ch/announce/or send an email to licensesiab-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 RLLSFRNYEHNTSVVKKIHLSVVDKANRDMASIVSEIMMYVLIVVLTIMIVAEMVYCYKK 184
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Mammalia, Butheria, Rodentia, Sciurognathi; Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                   Přaní Přůvolí; 1g; 1,
PROSTR: PSGASS; TG LIKE, PALSE NBG.
TOTIC charmel, Transmembrane; Ton transport; Voltage-gated channel;
Glycoprotein; Šígnal; Immungo, Rankinalff;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
SODIUM CHANNEL BETA-1 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND BRAIN.

-1. DISEASE. Defects in SCNIB are a cause of generalized opilepsy with febrile seizures plus (GEES-) [MIN.60433]. GEFS- is a disease characterized by a highly variable phencype combining febrile seizures, generalized estaures often precipitated by fever a age seizures, generalized seizures often precipitated by fever a age 6 years or more, and partial seizures, with a variable degree of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSEE SPECIFICITY: ABUNDANTLY EXPRESSED IN SKELETAL MUSCLE, HEART
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WARLANT GENERS TRP-12. The Med-9697698; Wellzer E.H., Ward D.H., Oberge A.L. Jr., Wellzer E.H., Warg D.H., Singh M. Scheffer I.E., George A.L. Jr., Berlace E.H., Warg D.H., Singh M. Schollsen E.H., Suberland G.E., Berlovic S. F., Mallac J.C., Berlovic S. F., Mallac J.C., Berlovic S. F., Mallac J.C., George A.L., Schollsen and generalized epilopsy associated with a mutation "Special sequence and generalized epilopsy associated with a mutation"
                   MEDLINES-SIFTIGE, PHEMEGROSAGES, AS ABMORGES, AS A GREELLA AS A. I., CARRON S.C., Slaugenhaupt S.A., Greella J.F., METRE-Cloning and expression of a sodium channel beta 1-subunit CDNA From human brain. *;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in the Na (4) channel becar, subunit gene SCHE.)

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Nav. Gener, 
                                                                                                                                                                                                                                                                 "Voltage-gated Na+ channel beta l subunit mRNA expressed in adult
human skeletal muscle, heart, and brain is encoded by a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genomic organization and chromosomal assignment of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005248; F:voltage-gated sodium channel activity; TAS. GO; GO:0006814; P:sodium ion transport; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      voltage-gated Na+ channel beta 1 subunit gene (SCNIB).";
Genomics 23:628-634(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Makita N., Sloan-Brown K., Weghuis D.O., Ropers H.-H.,
George A.L. Jr.;
                                                                                                                                                               SEQUENCE FROM N.A.
TISSUEHHeart, and Skeletal muscle;
MEDLINE-94171797; PubMed-812590;
MRKIR N., Bernett P.B. Jr., George A.L., Jr.;
Voltage-gated Nat channel bete 1, subunit mRNa
                                                                                                                                                                                                                                                                                                                                       Biol. Chem. 269:7571-7578(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95154833; PubMed=7851891;
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EMBL, L16242, AAA61277.1; -.
EMBL, U12193, AAB97608.1; -.
EMBL, U12189, AAB97608.1; JOINED.
EMBL, U12190, AAB97608.1; JOINED.
                                                                                                                    Hum. Mol. Genet. 2:745-749(1993).
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EMBL, U12192, PAB97608.1, 0
PR, A55734, A55734
Genew, HGNC.10586, SCNIB.
MIN, 600235, ...
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                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
   TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                   gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 EEFVKILRYENEVLQLEEDERPEGRVVWNGSRGTKDLQDLSIFITUVTYNHSGDYECHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 REFEFEAHRPFVKTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTLWLLIEMIYCYRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 RLLFFDNYEHNTSVVKKIHLEVVDKANRDMASIVSEIMMYVLIVVLIHLVAEMYKYKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 LALVVGAVLVSSAMGGCVEVDSETEAVXGMTPKILCISCKRRSETTAETFTEMTFRQKGT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKRBEVEATTVVEWFYRPEGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSTE: PSGGS15, IG LIKE, PALSE NEG.
IONIC channel, Transmembrane, Ion transport; Voltage-gated channel,
Glycoprocein, Signal, Immunoglobulin domain.
SIGMAL.
                                                                                             -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, HEART, SKELETAL MUSCLE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
-j- SUBGNIT: THE SOLIDM CHANNEL CONSISTS OF A PORE-FORMING ALPHA
SUBGNIT, BETA-1 AND BETA-2 SUBGNITS: BETA-1 IS NONCOVALENTLY
ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINKED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                            AND SPINAL CORD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.0%; Score 472; DB 1; Length 218; 49.1%; Pred, No. 2.6e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SODIUM CHANNEL BETA-1 SUBUNIT. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.1%; Pred, NO. 4.05.22,
tive 33; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBA84FC44FF2306B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 VSKA-EEAAQENASDYLAIPSENKEN-SAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-SEP-2093 (Rel. 42, Last annotation update)
Sodium channel beta-1 subunit precureor.
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24692 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003006; Ig MHC. Pfam; PF00047; ig; 1.
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135 1
218 AA;
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CIB1_HUMAN
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Matches
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 EBFVKILRYENBVLQLEEDERFEGRVVWNGSRGTKDLQDLSIFITNVTYNHSGDYBCHVX 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 REFERENBEVKTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTIWLLIEMIYCYRK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 RLLFFENYEHNTSVVKKIHIEVVDKANRDMASIVGEIRMYVLIVVLITHLVAEMIYCYKK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LASLVLIYWVSVCFPVCVBVPSETBAVOGNPMKLRCISCMKRBEVBATTVVEMFYRPEGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S LALVVGAALVSSACGGCVEVDSETEAVYGWTFKILCISCKRRSETNÄETFTEWTFROKGT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Gaps
                                                        Ionic channel, Transmenbrane, 107 Ltatisport, Voltage-gated channel, Signal, financoloulin domain; Disease mutation. Signal 18 munoslobulin domain; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CRUCIAL IN THE ASSEMBLY, EXPRESSION, AND FUNCTIONAL MODULATION OF THE HERFORFALBERT COMPLEX OF THE SOLD CHANNEL. THE BERT, I SUBUNIT CAN MODULATE MUTIFIED ALCHA SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammila, Eurheria, Rodentia, Schurognathi, Muridae, Musinse, Mus. McB. Texto-10090;
                                                                                                                                                                                                                                                                   (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
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STRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAINS-CSTRAI
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KXpershmidt S., Yang T., Roden D.M.;
"Rodalation of cartiac Na -current phenotype by betal-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 218;
                                                                                                                                           SODIUM CHANNEL BETA-1 SUBUNIT.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  41.9%; Score 471; DB 1; Length 218
49.5%; Pred. No. 3.2e-35;
ive 31; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR 010165.
24707 MW; 09B812FA3F9E9018 CRC64;
                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE.
POTENTIAL.
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N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
N-LINKED (GLCNAC. .
C -> W (in GEF8+).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [5-JUL-1998 (Rel. 36, Created)
(5-JUL-1998 (Rel. 36, Last sequence update)
(5-SEP-2003 (Rel. 42, Last annotation update)
GO; GO:0007266; P:synaptic transmission; TAS.
InterPro; IRR03006; Ig_MHC.
PFam; PF00047; ig_LIKE; FALSE_NEG.
PROSITE; PS50035; IG_LIKE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium channel beta-1 subunit precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Desc LOCAL Similarity 49.5%;
Matches 106; Conservative 3
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                                                                                                                                                                                                          218
150
121
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P97952;
                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
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Bukaryota; Wetaro: Chordata; Craniata; Vertebrata; Buteleor'omi;
Mammalia; Buteria; Rochenta; Sciurognathi; Muridae; Murinae; Rattus.
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ISOFORMS FROM BRAIN, SKELETAL MUSCLE, AND HEART (BY SIMILARITY).
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                                  -1- SUBGUIT: THE SOUTH CHANNEL CONSISTS OF A PORB-FORMING ALPHA
SUBGUIT: BETA-1 AND BETA-2 SUBGUITS: BETA-1 IS NORCOVALENTLY
ASSOCIATED WITH ALPHA, WHILE BETA-2 IS COVALENTLY LINESD BY
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                      DISULFIDE BONDS.

- SUBCELLOAR LOCATION: Type I membrane protein.
- SIMCELLOAR LOCATION: Type I membrane protein.
- SIMILARIY: CORTEAIN: I immunoglobulin-1 ke C2-type domain.
                                                                                                                                                                                                                                                                                                                        41.6%; Score 460; DB 1; Length 218; 48.6%; Pred. No. 6e-35;
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EXTRACELLULAR (POTENTIAL).
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01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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InterPro; IPR003006; Ig_MHC.
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-I- SIMILARITY: Cobtains 1 immunoglobulin-like V-type domain.
-I- SIMILARITY: BELONGS TO THE MYELIN PO PROTEIN PAMILY.
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SEQUENCE FROM N.A.
MEDLINE=85124601; PubMed=2578885;
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Neuron 1:73-83(1988).
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'TWA REQUEREC, gender C., Stahl N., FYRIDGE U., Popho B.;
'TWA REQUEREC, gender organization, and chromosomal localization of beolymorphic alaleal while protein zero general involutional control of polymorphic alaleal with the protein zero general myself of the protein cearing seconds or 1751,17919.

- FUNCTION: CREATION OR AN EXTRACELLULAR MEMBRANE FACE WHICH GUIDES THE MRAPHEN ROCCES NO UNITHATELY COMPACTS ADDITIONAL MATERIALS.

- INSURE SPECIFICATION TO THE MEMBRANE PROCESS.
                                                                                                                                                                                                                                                              15.6%; Score 175; DB 1; Length 248;
28.1%; Pred. No. 1.3e-08;
ive 34; Mismatches 99; Indels 18; Gaps
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10-RAC-1992 (Rel. 22, Last sequence update)
11-RE-2003 (Rel. 42, Last amnotation update)
Whyelin Po protein precursor (Myelin protein zero) (Myelin peripheral protein (MPP).
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Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 ALQRRISAMEKGKFHKSSKDSKRGRQTPV 218
                                                                                                                                                                                                                                                                                                                                 59; Conservative
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    127
105
108
109
112
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123
138
248 AA;
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WATANTS CAPT-1B GALO AND GALO-96.
Hayasaka K., Himoro M., Sato W., Takada G., Uyemura K., Shimizu N.,
Bird T.D., Commally P.M., Clamore P.R.;
Bird T.D., Commally P.M., Clamore P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Su Y., Brooks D.G., Li L., Lepercq J., Trofatter J.A., Ravetch J.V., Lebo R.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDLINGS-4015314, Pubbeds-753130,
WALTERS T. BOLINIS P.A. WOllerman R.A. Kemp S. Te Nijenhuis S. Walentjin L.J. Heneels G. W. Jennekens F.G., de Visser M., Moogendijk J.E., Baas F.J.
Polestickin G. He serrine 34 ockon From Leve major peripheral myelin procesn PO gene in Charce-Marie-Tooch disease type 18. ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelis E., Haites M., van Brocchikovan C.;
Hantations in the peripheral myelin genes and associated genes in
Hambatted peripheral myeling genes and associated genes in
Hambatted peripheral neuropathiss.";
                                                                                                                                                                                                                                                                                                                                                                                                                                Parel P.1., Lupski J.R.; "Charcot-Marie-Tooth disease: a new paradigm for the mechanism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94154677; Pubbed-1599289, Partie M.-G., Roeckel N., Pamelbin D., Forthi X., Blanquet P., Mattei M.-G., Roeckel N., Lattour P., Glazot G., Vandenberghe A., Dautigny A.; Lattour P., Clazot G., Vandenberghe A., Dautigny A.; Lattour P., Clazot G., Vandenberghe A., Dautigny A.; Lattoure and note of properties and president myells in protein are general service and chromosome 1021-1021-1021-1021-1031.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMARY CWT-18. CYG-22.
MEMARY CWT-18.
MEMARY CWT-18.
HIMOCO M., Yoshikawa H., Natoui T., Mitcui Y., Takahashi M.,
And M., Mahimura T., Sawaishi Y., Takada G., Haysaka K.;
Yaswa Matcion of the myelin Po gene in a pedigree of
Biochem. Wol. Skol. Int. 31:169-173 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94100991; PubMed=7516005;
Hayasaka K., Himoro M., Sawaishi Y., Nanao K., Takahashi T.,
Takada G., Nicholson G.A., Oluviter R.A., Tachi N.;
                                                                                                                                                                                                                                                    MEDLINE-95282670; PubMed-7762451;
Roa B.B., Lupski J.R.,
"Molecular genetics of Charcoc-Marie-Tooth neuropathy.";
Ador. Hum, Genet. 22:117-152(1994);
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Mol, Genet. 2:1369-1372(1993).
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MEDLINE=99103460; PubMed=9888385;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rends Genet. 10:128-133(1994).
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Nat. Genet. 5:31-34(1993)
                                                                                                                                                                                                                            REVIEW ON CMT-1B VARIANTS
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.3%; Score 172; DB 1; Length 248;
clarity 28.1%; Pred, No. 256-08;
Conservative 34; Mismatches 99; Indels 18; Gaps
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10-WAY-1952 (Rel. 22, Last sequence update)
10-WAY-1952 (Rel. 22, Last sequence update)
10-WAY-1950 (Rel. 42, Last amnocation update)
10-Well ne procein precursor (Myelin protein zero) (Myelin peripheral
10-Well (MRP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Isolation and sequence determination of cDNA encoding the major structural protein of human peripheral majoristim", Brochem a Brophys. Res. Commun. 180:515-518(1991).
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Agyasaka K., Nanao K., Tahara M., Sato W., Takada G., Miura M.,
Dyemura K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .) (COMPLEX)
                                                                                                                                                                                                                                                        Phosphorylation, Immunoglobulin domain; Signal.
Signal. 1 29 BY SHILARITY.
SIGNIN 30 248 MYELIN PO PROTEIN.
DOMAIN 30 153 EXTRACELLULAR (BY SIMILARITY).
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CYTOPLASMIC (BY SIMILARITY).
                    MOD (MG111011777) Wp. Three-Pro) PRO0111011777 Wp. Three-Pro) PRO01916 / 42-like.
Inter-Pro) PRO01916 / 42-like.
Inter-Pro) PRO01916 / 42-like.
Inter-Pro) PRO01916 / 42-like.
SWARTY, SROO161 / 47-like.
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TISSUE-Spinal cord;
                                                                                                                                                                                                                                                                                                                                                                                                           IG-LIKE V-TYPE.
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        HSSP; P06907; 1NEU
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AC P25189; Q16072;
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"Two divergent types of nerve pathology in patients with different PO
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"Clinical phenoryse of different MPF (TO mittations may include
Clinico-Marie-Tookh Uppe 18, Dejetine-Soctas, and congenital
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Chance P.F., Lupski J.R.
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                                                                                             JARIANTS CMT-18 LEU-78 AND ASN-134.
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71 DFL-IYEYRNGHQEVE--SPRQGRLQWNGSKDLQDVSITVLMVTLNDSGLYTCNVSREFE 127
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granish ancestry with Chronoch-Mark-Tooth disease and hereditary
neuropathy with liability to pressure palases.";
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11-UUI-1999 (Rel. 11, Last sequence update)
11-SBL-100 (Kel. 14, Last asquence update)
11-SBL-100 protein (Wellin protein zero) (Wyelin peripheral protein)
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Rommalia; Butheria, Bos. Cetarticodactyla; Ruminantia; Peccra; Bovoidea;
Romanalia; Bos.
        VENTANT CMT-1B GUU-93.
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SOYOUR E. Mecmillan J. Updokhaya M.;
SOYOUR D. Mecmillan J. Updokhaya M.;
                                                                                                                                        VARIANT CMT-1B LEU-78, AND VARIANT DSS CYS-98.
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                                                                                    Marie-Tooth disease type 1B,";
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Best Local Similarity
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Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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Interpro; 1FR00110; 13-13ke.
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Interpro; 1FR003566; 1g,V.
InterPro; 1FR000520; Myelin_Po.
Pfam; PF00047; ig; 1.
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215 AA;
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Peritani M., Teesalu T., Consaler G.G., Ofreasi F.,
Petitaliani M., Teesalu T., Consaler G.G., Ofreasi F.,
Petitaliani M., Peesalu T.,
Petitaliani M., Peesalu T.,
Petitaliani M., Appressed in embryonic epithelia With a potential Yole as
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
-!- TISSUE SPECIFICITY: FOUND ONLY IN PERIPHERAL NERVOUS SYSTEM
                       POTENTIAL.
N-LINKED (GLCNAC. . .) (COMPLEX)
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PROSITE; PESOBS, IG_LIKE; 1.
PROSITE; PESOBS68; MELIN PO; 1.
Myelin; Structural protein; Glycoprocein; Transmembrane;
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PHOSPHORYLATION (BY PKC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE V-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation; Immunoglobulin domain.
DOMAIN 1 124 EXTRACELLE
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                                                                                                PR. N.2128 A.9128

1859 Pr6607 NR186

(NrcoSultedB) N10527 -11ke.

INCEPTO IPRO1006 19_MEC.

INCEPTO IPRO1006 19_MEC.

INCEPTO IPRO10969 19_M.
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MEDLINE=98252857; PubMed=9585423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 HKTAKDASKRGRQTPV 189
                                                                                                                                                                                                                                                  Pfam; PF00047; ig; 1.
PRINTS; PR00213; MYELINPO.
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219 AA;
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homotypic adhesion molecule in thymus histogeneeis.";

1. Cell Bit. 141.1021.1031.103

1. SURCINI: Heddates homophilic cell-cell adhesion

1. SURCINI: Heddates homophilic cell-cell adhesion

1. SURCINI: Moldates homophilic cell-cell adhesion

1. SURCINI: Moldates homophilic cell-cell adhesion

1. SURCINI: SPECIFICITY: Expressed in liver and gut, skin, and testis

1. Dur not in thymocytes, lymphocytes, macrophage or dendrific cells

0. Cell-lines
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spatris, swoodeds, Idv; 1.
PROSITE; SPOGESS; ILV; ILVES; I. Transmembrane; Glycoprotein;
PROSITE; Adhesion; Usamunoglichlin domain; Fransmembrane; Glycoprotein;
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1G-LIKE U-TIPE.
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
FGEERRA'FRITE (GLCNAC. . . ) (POTENTIAL).
FGEERRA'FRITE (GLCNAC. . . ) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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23.4%; Pred. No. 2.4e-06;
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28-F8B-2003 (Rel. 41, Last sequence update)
15-58P-7003 (Rel. 42, Last samotation update)
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68 LDGGPEOFFVFYHIDPFQPMSGRPKDRVSWDGNPERYDASILLMKLQPDDNGTYTCQVKN 127
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35; Mismatches 80; Indels 50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myelin PO protein precursor (Myelin protein zero) (Myelin peripheral
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Bukaryota, Metacar (hordata, Cranista, Vertebrata, Chondrichthyes,
Blambytanchii, Galescopphii, Heterodontoidea, Heterodontiformes,
Heterodontidae, Heterodontus.
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PSS0815; IG LIKE: 1.
Cell adhesion; Immunoglobulin domain; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (FOTENTIAL).
IG-LIKE VITYEE.
BY SINLIARIES (GLUCHAC. . ) (FOTENTIAL).
N-LINKEE (GLUCHAC. . ) (FOTENTIAL).
N-LINKEE (GLUCHAC. . ) (FOTENTIAL).
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-- SIMILARITY: CORLAINE I Immunos]cbolin-like V-type domain.
--- SIMILARITY: BELONSS TO THE MYELIN PO PROTEIN FAMILY.
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Pred. No. 3.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPITHELIAL V-LIKE ANTIGEN 1.
EXTRACELLULAR (POTENTIAL).
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15-SEP-2003 (Rel. 42, Last annotation update)
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         Theerpro; IPPRO0710; Ig-like.
INTERPRO; IPPRO07105; Ig_MRC.
INTERPRO; IPPRO07595; Ig_W.
PEAM, PPRO047; Ig; I.
SMRNYS; PRO0713; MELLNPO.
SWART; SMO0465; IGY. I.
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TISSUE-Sequency: A. Petersen I., Sebluona K., Petersen S., French M. S., Petersen I., Sebluona K., Petersen S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S., September M. S
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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GO:0007345; P:embryogenesis and morphogenesis; TAS.
GO:0007345; P:homophilic cell adhesion; TAS.
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databaseg.
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J. Neurosci. Res. 25:143-151(1990)
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swise Institute of Bioinformatics and the Emel outsitution the Emergan Bioinformatics Institute. There are no restrictions on its use by non-this office institutions as forg as its content. So in no way modified and this other accessent is no removed. Usage by and for connectal entities requirement is not removed. Usage by and for connectal or sent an email to licensessible sib.ch).
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                                                                                                                                                                                                                                                    69 DNSRDIISIFHYGNGVPYIEKWGQPRGRVEWVGDISKABGSIVIRNLDYIDNGTFTCDVK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LFCCSVLYAPSVLRPSQGISVSTHHNLHKTVGSDVTLYC-GFWSNBYVSDLTLSWRFRP 68
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Thus gallue (Chicken),
Enkaryceia, Metazas, Gordata, Cramiata, Vertebrata, Buteleostomi,
Sulsania, Mesa, Moogmathes, Galliformes; Phasianidae, Phasianimae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Mismatches 77; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-CCT-1994 (Rel. 10, Last sequence update)
115-582-2003 (Rel. 42, Last montation update)
Wyelin PO, porcean precursor (Myelin protein zero) (Myelin peripheral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             operine; P85083; NG_LIKB; 1.
PROSTER; P800589; NG_LIKB; 1.
PROSTER; P800589; MTELIAN PO: Wellia; Transmembrane; PRospborylation; Immunoglobulia domini; Transmembrane; PRospborylation; Immunoglobulia domini; Transmembrane; PROspborylation; Immunoglobulia domini; Transmembrane; TGRANL TRANSMEMBRANCE; PROSPERGANCE;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA; 27335 MW; A776A9ED9D430FA0 CRC64;
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72 GSRDSISIFHYGKGQPYIDDVGSFKERMEWVGNPRRKDGSIVIHNLDYTDNGTFTCDVKN 131
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- I- FRONÇTION: CREATION OF AN EXTRACELLULAR MEMBRANE REGENTION GUIDES THE MARPENS PROCESS AND ULTIVATELY COMPACTS ADANCENT LANGLAG. I- SHERELLAR. LOCATION: P.P.G. I membrane process.

- I THESE SPECIFICITY: FOODD ONLY IN PERITHERAL MERVONS SYSTEM.
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Rattaryosa Metazos, Chordata/ Craniata; Vertebrata; Buteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinee, Rattus.
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127 POTENTIAL.
122 N-LINKED (GLUNAC. . .) (POTENTIAL).
27466 WM; FBD14801FP8A08FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 30-58; 95-134 AND 142-151.

SEGUENCE-SPOCKALL; PRUMBARS 251.471.

SEGUENCE-SPOCKALL; REMARE SEGUENCE, WESTERDFOOK R.E.,

SEGUENCE, SCHOLE T., CRITERIAL W.A.,

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-- STMILANTY: Contains 1 immunoglobulin-like V-type domain.
-- SIMILANTY: EBLUNGS TO THE MELLIN PO FROTEIN PAMILY.
-- HASP, FAGIOR7.
-- HASP, POGGO7, NED.
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12.5%; Score 140.5; DB 1, Length 2
Best Local Similarity 23.6%; Pred, Mo. 1.7e-05;
Matches 48; Conservative 43; Mismatches 67; Indels
Atches 48; Conservative 43; Mismatches 67; Indels
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01-OCT-1996 (Rel. 34, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sodium channel beta-2 subunit precursor.
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EMBL; M86441; AAA37286,1; -.

P21803; O55141; Q00389; Q61342; 01-MAY-1991 (Rel, 18, Created) 01-NOV-1997 (Rel, 35, Last sequence update)

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whis swiSe-spore entry is copyright. It is produced through a collaboration between the Swise Institute of Skiniformatics and the BWHs outstation the Bwesness the Swise Institute of Skiniformatics and the BWHs outstation the West Pyr map sporify institutions as longs as the contemn of some varieties are activated and this statement is now removed. Usage by and for commercial entities required allocates agreement (See Netp.//www.iab-sh.ch/announce/or sends an enail to litersessib-sh.ch).
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Normable Tyrosine Kinase identified by phosphoryrosine antibody
screening of CDMA libraries "H.
Hol. Cell Biol. 8:5541-5544 (1988).
Hol. Cell Biol. 8:5541-5544 (1988).
FOURTHER RECEPTOR FOR ACIDIC TRIAN FOR BISIC FOR STORY
POGESSISS A HIGHER APPRINTY FOR ACIDIC TRIAN FOR BISIC FOR STORY
TO ANALYTIC ACTIVITY: ATP + a procein tyrosine = ADP + procein
Fibe-Spa, 2001 (Rel. 42, Last emocation update)
Fibe-Spa, 2001 (Rel. 42, Last emocation update)
(Kexatinoto) growth factor receptor 2 produceor (RC 2.7.1.112) (FGFF-2)
FFFR 20 R DFH BRK.
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'TONGS.R.F., BERTE N.D., Oldridge, 'Heath J.K., Wilkie A.O.M.;
'TONGS-TONG OF ONG-CANOMICAL 5' Splice site (/GA) in alternative
splicing by fibroblast growth factor receptors 1, 2 and 3.";
Hem. MOJ. Gener. 7;655-691(1998).
                                                                                                                                                                                                                                                                                                                                                                                              ssQUENCE FROM N. (15OPCWAN LOXA).
STRAINSALAGO; TISSGUESPRIN;
NEDLINE-91270892; DANDWAG-1211190,
NRC V. Kelman Z. Ravivi A. Newfeld G., Givol D., Yarden Y.;
NRC V. Kelman Z. Ravivi A. Newfeld G., Givol D., Yarden Y.;
PGC. Mased identification of new receptors: molecular cloning of a receptor for fibrolisat growth factors: ";
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Isoid-P21803-2; Sequence-VSP 002985, VSP 002986, VSP 002987;
-!- SIMLAITY; BELONGS TO THE FIBROBLAST GROWTH PACTOR RECEPTOR
                                                                                                                                                                                                                                                                                    "Characterization of the murine BEK fibroblast growth factor (FGF) receptor: activation by three members of the FGF family and
                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM SHORT).
MEDLINE-2103597; PubMed-1246048;
Miki T., Flaming T.P., Bottaro D.P., Rubin J.S., Ron D.,
Aaronson S.A.;
                                                                                                                                                                                                                                                   Mansukhani A., Dell'Era P., Moscatelli D., Kornbluth S.,
Hanafusa H., Basilico C.;
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Proc. Natl. Acad. Sci. U.S.A. 89:3305-3309(1992).
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MEDLINE=89219016; PubMed=2468999;
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MEDLINE=92228773; PubMed=1373495;
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                                                                                        Mus musculus (Mouse)
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FIBROBLAST GROWTH FACTOR RECEPTOR 2. EXTRACELLULAR (POTENTIAL).
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279 KVYSDAQPHIQMIKHVEKNGSKNGPDGLPYLKVLKAAGVNTTDKEİBVLYIRNVTPEDAG 338
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Query Match
9.9%; Score 111.5; DB 1; Length 821;
Best Local Similarity 25.9%; Pred. No. 0.025;
Matches 41; Conservative 23; Mismatches 55; Indels 39;
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MYGOGANGCANLTULRKQG (in isoform Short).

A - V (IN REP. 2).

G - N (IN REP. 2).

I - Y (IN REP. 2).

DV - R (IN REP. 2).

C - V (IN REP. 2).

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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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                                                                                            December 5, 2003, 22:55:42; Search time 109 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

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Result No.	Score	% Query Match	% Query Match Length DB	DB	SUMMARIES ID Desc	Description
7	1124	100.0	230	4	Q9ULR2 Q9ul	Ogulr2 homo gapien
2	1116	99.3	215	9	Q8HXJ7 Q8hx	28hxi7 macaca fasc
۳	1105	98.3	215	13	C93K00	091k00 rattus norv
4	1097	97.6	215	7	QBBHK2 08b	Sebaka mus musculu
2	1091	97.1	215	Ξ	Q91299 Q91	Q91299 mus musculu
9	420	37.4	185	4	Q8WU42 Q8wu	Q8wu42 homo gapien
7	262.5	23.4	273	11	60 EUXQ60	Q9qxu3 rattus norv
80	178.5	15.9	203	13		OBife6 brachydanio
6.	163.5	14.5	251	4	0	014902 homo sapien
10	163.5	14.5	258	4	Q9BR67 Q9br	29br67 homo sapien
11	160.5	14.3	225	4		292677 homo sapien
12	150	13.3	202	13		091406 salmo sp. i
13	147	13.1	215	11		091wi4 mus musculu
14	147	13.1	229	13		D8avm3 xenopus lae
15	131	11.7	243	4	Q9UEL4 Q9ue	Q9uel4 homo sapien
16	131	11.7	269	4		395297 homo sapien

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111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Q9UEL6	Q9NYK4	08JG36	QBIX11	QSIX39	Q9D7B8	062861	QSIX38	QBK1G0	Q8R373	Q9TTZ3	092085	Q8N917	099052	09н6в4	061563	Q96MJ0	096KV6	Q9R293	Q63241	Q63242	931406	063237	Q8NF70	QBUWK1	Q8UML1	Q91WP1	Q8K094	QBBVF6
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Titt o googood eeee	11.3	11.3	11.1	11.1	10.9	10.8	10.4	10.3	10.3	10.2	6.6	9.6	9.7	7.6	7.	9.6	9.50	5	9.3	9.2	9,2	9.5	9.5	9.1	8.9	8.9	8.8	8.8	8.8
	127	127	125	125	122	121	117	116	115.5	114.5	111.5	110.5	109	109	108.5	101	106.5	106.5	104.5	103.5	103.5	103.5	103.5	102	99.5	99.5	98.5	98.5	98.5
	17	18	13	20	23	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapidam (Human).
Bukaryota, Netazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Nemmalish Eutheria; Frimates; Catarthini; Mominidas; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

100.04; Score 1124; DB 4; Length 230;
Best Local Similarity 100.04; Pred. No. 11e-109

Matches 215; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 AA; 26357 MW; B06D5155E5FB5F98 CRC64;
                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TEMBHILE). 13, Last sequence update)
MARR-2003 (TEMBLICE). 23, Last annotation update)
Mypothetical protein KIAA1158 (Fragment).
                                                                                                                                            230 AA.
                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                 PRT;
                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA1158.
                                                                                                                                 Q9ULR2
RESULT 1
                                                                Q9ULR2
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1 MPAFNELFPLASLULIYWVSVCPPVCVFUPSETEAVQGNPMKLRCISCMKREEVBATTVV 60

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61 EMPYRPEGGKDFLIXEYRNGHQEVESPFQGRLQMNGSKDLQDVSITVLNVTLNDSGLYTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MENDINE 2015(048, PAMEAL 106894) COX P. DIXON A.K., Lee K., Permock E. D., Elder B. B. Shaw B., Cox P. DIXON A.K., Jee K., Permock E. D., Hidhes D. A., Richardson P.J., Mixauguchi K., Jackson A.P.; Permock E. D., Hidhes J., Richardson P.J., Mixauguchi K., Jackson A.P.; Permock E. B., Hidhes M. M. Shamel Jackson With Jackson Elemstrian Codium Canamael Later lower with distrinct kinetics."; Proc. MEI. Acad. Sci. U.S.A. 97:3308-2313 (2000).
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                                                                                                                                                                                         Rattus norvegicus (Rat).
Rattus norvegicus (brotats, Craniats, Vertebrata, Buteleostomi;
Mammalia, Butberia, Rodentia, Sciurognathi, Muridae, Mutinee, Rattus.
01-MAR-2003 (TREMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mamalia, Butheria, Rodentia, Sciurognathi, Muridae, Murhae, Mus. MCR. Taxila.10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINS-grandup-Dalayory ITSSING-Dorsal voor gandjinden P.S., 
Slice-Sartiago I., Catterall M.A., Scheuer T., 
Differential Modulation of Sodium Channel Geting and Persistent 
Sodium Currents My the Decal, Deta?, and Deta3 Subunites."; 
Exbmitted (MWY-2001) to the EMEJ/GenBank/DDSJ databases. 
BMBI, Arya33359, CARS6381.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 AA; 24799 MW; 056B48BEF5EAEF4F CRC64;
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01-WAR-2003 (TrEMBLrel. 24, Last annocation update)
101-kage-gated sodium channel beta-3 subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 YRKVSKAEEAAQENASDYLAIPSENKENSAVPVEE 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P06907, INEU.
InterPro; IPR003599; IG.
InterPro; IPR00110, IG-like.
InterPro; IPR003006; IG MHC.
PEam, PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG LIKE; 1.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART, SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                                                    SCN3B OR SCNB3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissum-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                              61 EMFYRPEGGKOFLIYEYRNGHQEVESPFQGRLQMNGSKDLQDVSITVLNVTLNDSGLYTC 120
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                                                                                                                                                                                                 76 EWFYRPEGGKDFLIYEYRNGHQEVESPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTC 135
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       16 MPAFNRLFPLASLVLIYWVSVCFPVCVBVPSETBAVQGNPMKLRCISCMKRBEVBATTVV 75
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MeDINE-2448951; Pubwed-11574149;
Miral M.; Parao M.; Suxukl Y.; Osigano S.; Bashimor M.; Suro Y.;
Hiral M.; Parao M.; Suxukl Y.; Osigano S.; Bashimor M.;
Hiral M.; Parao M.; Suxukl Y.; Osigano S.; Bashimor M.; Suro Y.;
Miral M.; Parao M.; Osiwik J. Osigano S.; Bashimor M.; Suro M.; Suro Y.; Osigano S.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.; Suro M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca Esscioularis (Crab eating macaque) (Cynomolgus monkey).
Modrayota; Meteraca; Chordata; Craniata; Vertebrata; Buteleoeromi;
Mommalia; Butheria; Primates; Catarrhini; Cercoptrhecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE-Wedulla oblongata,
Hachimoco K., Osada N., Hida M., Kusuda J., Sugano S.;
Hachimoco K., Osada N., Hida M., Kusuda J., Sugano S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 275:31-37(2001).
BRBU, AB097521, BAC41746.1; -.
Hypotherical protein.
SEQUENCE 215 AA, 24702 MW, 25319D5ED218AACF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2003 (TrEMBLrel, 23, Created)
O1-MAR-2003 (TrEMBLrel, 23, Last sequence update)
O1-WAR-2003 (TrEMBLrel, 23, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        093000,
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 YRKVSKAEEAAQENASDYLAIPSENKENSAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YRKVSKAEBAQBNASDYLAIPSENKENSAVPVEE 215
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156 VVSEIMMYILLVPLTIMILLIEMIYCYRKVSKA-BEAAQENADYLAIDSENKRN-SAVPV 213
124 IVSEIMMYILLVPLTIMILNEMIYCYRKASATTETAAQENASEVIAITSESRSKENGVY 183
124 IVSEIMMYILTVITIMILMEMIYCYRKASATTETAAQENASEVIAITSESRSKETVOV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98 --KDLQDVSITVLNVTLNDSGLYTCNVSREFEFEAHRPFVKTTRLIPLRVTBEAGEDFTS 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 KIRCISCMKREEVEATTVVEWPYRPEGGKDFL-IYEYRNGHQEVESP--FQGRLQWNGS- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 KILCÍSCKRKSÉTNÁETFTÉWTFROKGTEEFVKILRYENEVLOLÉEDERFEGRVVWNGSR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Gordata, Craniata, Vertebrata, Buteleostomi, Mamalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. Mamalia, Taxil-10116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEDIJINE-200928777, Pubwed-10625649,
Rezur-Callaeple K.L., Pagedate D.S., D'Andrea M.R., Mattei L.N.,
Negere K.E., 18cm L.L.,
"Cloning, Jocalization, and functional expression of sodium channel
Decila subunits":
                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strandberg R.; Submitted (1MV-2002) to the EWEL/GenBank/DDBJ databases. Submitted (1MV-2002) to the EWEL/GenBank/DDBJ databases. Increpro. 12001306 Mg12266.1; Pfan. PPRO047; 19.71. Spr. Mg1. Spr. Mg1. Spr. Mg1. Spr. Mg1. CFSEB8510DC59800 CRC64; Spr. Mg1. CFSEB8510DC59800 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                     181 YRKVSKABBAAXBNASDYLAIPSENKENSVVPVBE 215
              181 YRKUSKAEEAAQENASDYLAIPSENKENSAVPVEE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 37.4%; Score 420; DB 4; Local Similarity 49.5%; Pred. No. 6.4e-36; nes 90; Conservative 30; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Voltage-gated sodium channel subunit betai-A.
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01-NAY-2000 (TEMBLrel. 13, Last sequ
01-NAR-2003 (TEMBLrel. 23, Last anno
                                                                                                                                                                                                                                Created)
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EMBL, AF182949, AAF25186.1; -.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2002 (TrEMBLrel. 22,
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                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                Hypothetical protein.
Homo sapiens (Human).
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                                     the NIKEN Genome Exploration Research Group Phase I & II Toun;
"Analysis of the mouse transcriptome based on functional annotation of
"Analysis of the mouse transcriptome based on functional annotation of
Nature 400 553-573 (2002).

Nature 400 553-573 (2002).

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Mammalla; Butheria; Rodentia; Schurognathi; Muridae; Murinae; Mus
NCBI_TRAID=10090;
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                                                                                                                                                                                                                                97.6%; Score 1097; DB 11; Length 215; 97.7%; Pred. No. 6.7e-107;
                                                                                                                                                                                                                                                                             5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen C., Avery C., Kazen-Gillespie K., Isom J.L.;
Whouse brain and heart beta 3 sodium channel CDNA.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY049036; AAL07512.1;
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001202.2001 (TrawBirel 19, Created)

01-002-2001 (TrawBirel 19, Last sequence update)

01-0042-2003 (TrawBirel 13, Last amnocation update)

Erain and heart sociium chammel beta 3 subunit.
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                                                                                                                                                                                                                                                                                 0; Mismatches
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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SMART; SM00409; IG; 1.
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135 -----IVGKTSQVTLYVFEKVPTRYGVVLGAVIGGVLGVVLLLLLEFYVVRYCMLRRQA 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 SSLVL----SPAQAIVVYIDREVHGAVGSRVTLHC-SFWSSEWVSDDISFTWRYOPEGGR 74
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WITHOUTES-251345; PROMED-15-2052.
WAS Broced-Moven C.; Crahl H., Pfeiffer R.A., Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; Van Broced-Moven C.; V
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Mataryota, Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi,
Mammalia; Butheria; Primates; Catarrinin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IINTERPO: IRPO03056, 19_WRC.
INTERPO: IRPO03056, 19_WRC.
INTERPO: IRPO03056, 19_WRC.
INTERPO: PRO0319, WRELIND.
IRPUND: PRO0319, WRELIND.
IRPUND: PRO0319, 10_INTELLIND.
IRPUND: PRO0319, 10_INTEL.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MRA-2003 (TrEMBLrel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                  Last sequence update)
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                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrcl. 01,
01-NOV-1996 (TrEMBLrcl. 01,
01-MAR-2003 (TrEMBLrcl. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 28.3
Matches 54; Conservative
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                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                             Myelin protein zero.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Q9BR67;
                                                                                                                                                                                                   Q14902
Q14902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 KDAISIFHYGGGBAYPANKGPFQNRLEFVGNPSRRDGSILIKNLDFGDNGTFTCDAKNPP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 BFEAHRPFVKTTRLIPL-RVTEEAGEDFTSVVSEIMMYILLV----PLTLWLLJEMIYC- 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 DIGGH---PSTIRLLVPEKVPVQAGVITGSIIGVVLGLLILVVAIYYLMRFLVARRVFSL 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 KDFL-IYEYRNGHQEVESP--FQGRLQWNGS---KDLQDVSITVLNVTLNDSGLYTCNVS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 EEFVKILRYENEVLQLEEDERFEGRVVWNGSRGTKDLQDLSIFITNVTYNHSGDYBCHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 LISVVLLGIASQSTALVVNTDSEKHALVGSDVRLSC-SFFSWQWTSPEVSFTWHYRPDGA 65
                                                                                                                                                                                                                                                                                                                               10 LASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVVEWFYRPEGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVBATTVVEWFYRPEGG 69
                                                                                                                                                                                                                                                                                                                                                                                                       5 LALVVGAVLVSSAWGGCVEVDSETEAVYGMTFKILCISCKRRSETTAETFTEWTFRQKGT 64
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brachydanio rerio (Zebrafiah) (Danio rerio).

Bukaryota, Mesacas, Chordata, Grantata, Vertebrata, Buteleostomi,
Actinoptenygii, Meopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidee, Danio.

Reg. Taxib.?955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 REFEREAURPFVKTTRLIPLRVTEEAGEDFTSVVSEIMMYIL----LVFLTLM 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 15.9%; Score 178.5; DB 13; Length 203; I Similarity 26.9%; Pred. No. 1.6e-10; S3; Conservative 41; Mismatches 86; Indels 17;
                                                                                                                                                      Query Match 23.4%; Score 252.5; DB 11; Length 273; Best Local Similarity 39.3%; Pred, No. 156-19; Matches 69; Conservative 23; Misacches 53; Indele 29; Matches 69; Conservative 73; Misacches 73; Indele 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Shweitzer J., Becker T., Becker C.G., Schachner M.;
"Increased expression of protein zero (10) in the CMS during
regeneration of axons in adult zebrafish.";
Submitted (JUN-2002) to the EMEL/GenBank/DDBJ databases.
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PRATYS PROO13; MITELIANO
SRART; SROO406; 105,11
PROSTICE SROO406; 106,11
PROSTICE PEROBS; TO LIKE; 1
SEGUENCE 203 AA; 2207 MM; 12614E8076B373DL CRC64;
                                                                              273 AA; 31063 MW; 156A31899A906849 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-1667,
08-1667,
01-067-2002 (TrEMBLrel, 22, Last sequence update)
01-047-2003 (TrEMBLrel, 23, Last sequence update)
01-04R-2003 (TrEMBLrel, 23, Last annotation update)
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Pfam; PF00047; ig; 1.
Ionic channel.
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                                                                                    SEQUENCE
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                                                                                                                                                                                                                                84 VE--SPFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTCNVSRBFBFBAHRPFVKTTRLI 141
                                                                                                                                                                                                                                                                                                      66 IDEVGTFKERIQWVGDPR#KDGSIVIHNLDYSDNGTFTCDVKNPPD-----IVGKTSQV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 NDSGLYTCNVSREFEFEAHRPFVX.--TTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IVVYTDREVHGAVGSRVTLHC-SFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPY 65
                                      25 VCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVVEMPYRPEGGKDFL-IYEYRNGHQE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 LPPLASLVLIYWVSVCFPVCVBVPSRTEAV------QGNPMKLRCISCMKREEVE 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 PLRVTEBAGEDFTSVVSEIMMYILLVFLTLWLLIEMI-YCY-----RKVSKAEE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 TLYVPEKVPTRYGVVLGAVIGGVLGVVLLLLLLFYVVRYCWLRRQAALQRRLSAMEK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81, Indels 32, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmo, Bukaryota, Metazaa, Chordata, Cramiata, Wertebrata, Buteleostomi; Actinopterygii, Neopterygii, Teleostei; Buteleostei; Proteanthopterygii, Salmoniformes; Salmonidas; Salmo. vytel. Yextineoliji,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 202;
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SEQUENCE 202 AA; 72322 MW; 92C2900701B6E1E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.3%; Score 150; DB 13; 22.1%; Pred. No. 1.6e-07; ive 49; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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01-DEC-2001 (TrEMBLrel. 19, Created)
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Best Local Similarity
Matches 46; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 DFL-IYEYRNGHQEVE--SPFQGRLQMNGSKULQDVSITVLNVTLNDSGLYTCNVSREFE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREBVEATTVVEWFYRPEGGK 70
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Wall B. T. Immerman V. De Jonghe P., Muylle L., Martin J.,

Van Breckhoven C. (*).

Lichage and mutation analysis in an extended family with Charcot-
Marker-Corch diseases (type LR.

Simbnited (WAY-1994); Co. the EMBL/GenBank/DDBJ databases.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
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No. 1.49-08; Pp. 27; Pp. 27; Mismatches 77; Indels 19; Pp. Conservative 37; Mismatches 19; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; Pp. 20; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 14.5%; Scoxe 163.5; DB 4; Length 2 1 Similarity 26.3%; Pred. No. 8.1e-09; Indels 4; Conservative 33; Manaacches 91; Indels
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO06491; AAHO6491.1; -.
HSSP; P06907; INEU.
                                                                                                                                                                                                                                                                                                                                                            PÉGNI PÉPOLOST, 15.7.

PERTITA'S PRODOST, 15.7.

PERCITS, PROSOSS, 10.7.

PROCITE, PROSOSS, 10.11E2, 1.

PROCITE, PROSOSS, 10.11E2, 1.

PROCITE, PROSOSS, 10.11E2, 1.
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01-MRA-2003 (TrEMBLrel. 23, Last annotation update)
M30or peripheral myelin protein (F0) (Fragment).
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PRINTS, RRO213, WRELINPO.
SWART, SMOO4G; IGV, 1.
PROSITE; PSC0856, IG LIKE, 1.
PROSITE; PSC0568; WYELIN_PO; 1.
                                                                                                                                                                  InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
InterPro; IPR00920; Myelin_Po.
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InterPro; 19800306; 19 MHC.
InterPro; IPR003596; 19 V.
InterPro; IPR00920; Myelin_Po.
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                                                                                                                                                                                                                                                                                                                                                                     14 VLIYWVSVCFPV-CVEVPSETEA--VQGNPMKLRCISCMKREEVEATTVVEWFYRP-EGG 69
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                           th 13.1%; Score 147; DB 13; Length 229; Similarity 56.8%; Pred. No. 38e-07, S. 7; Conservative 35; Mismatches 93; Indels 21
            Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases. BMBL; BC041735, AAH1735.1; -. BMBL; BMBL; BMBL; BMBL; BMBL; BMBL; BMBL; BMBZGIEGE CRC64; SEQUENCE 229 AA; 25865 MM; 986A3E14BB2GIEGE CRC64;
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Rhodes S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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01-MX-2000 (TEBRERE) 13, Last sequence update)
01-MX-2003 (TEBRERE) 23, Last amortation update)
None septens (Muman) (Fragment)
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Best Local Similarity
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SEGURNOR FROM N.A.
SEGURNOR CONTROL TISSUE-Mesonephros;
Hebbline-2218(63): Indived-1246683;
The PARKON CONTROL TISSUE-Mesonephros
Hebbline-2218(63): Indived-1246683;
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                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kanopus Jaevis (African clawed frog).
Bukaryota, Netazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Amphiba; Barzachia, Amura, Mesobarzachia; Pipolada; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.1%; Score 147; DB 11; Length 215; 23.4%; Pred. No. 3.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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Pfam; PP00047; 4159; 1.
PRATYS; PR00213; MRZLINPO.
PRATY; SM00406, IGV; 1.
PR0SITE; PS50835; IG LIKE; 1.
PR0SITE; PS50835; AA; Z4092 MM; PGESE36787CF79C4 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; 18007110, 1g-like.
InterPro; 18003106; 1g MHC.
InterPro; 1800356; 1g V.
InterPro; 18000820; Myelin Po.
                                                                                Spithelial V-like antigen.
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Klein S., Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                   FISSUE=Salivary gland;
                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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173 DYTGCSTSESLSPVKQAPRKSPSDTBGLVKSLPSGSHQGPVI 214 임

Search completed: December 5, 2003, 23:22:33 Job time : 112 secs

Mon Dec

us-09-936-680-2.rai

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 5, 2003, 23:17:13; Search time 30 Seconds (without alignments) 333:228 Million cell updates/sec

1124 1 MPAFNRLFPLASLVLIYWVS......SDYLAIPSENKENSAVPVEE 215 US-09-936-680-2 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 Total number of hits satisfying chosen parameters: 328717 segs, 42310858 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the sors of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	App	Appli	Appli	Appli	appli	Appl	Appli	Appl	Appl	App,	, App	Appli															
g	389,	7,	4,	٥	6	44,	48,	42,	46,	18,	20,	22,	24,	56,	28,	30,	32,	34,	36,	38,	40,	~	13	20,	422,	503,	,
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APPLICATION NUMBER: 60/090694 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091626 PILLING DAIR: 1998-07-02 APPLICATION NUMBER: 60/091633 FILLING DAIE: 1998-07-02 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 APPLICATION NUMBER: 60/090540 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090542 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-06-24 FILING DATE: 1998-07-02 DATE: 1998-06-17 ### 100 PH 100 P PRIOR m

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APPLICANT: Zhao, Zhizhuang
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CURRENT PLING DATE: 1999-10-29
NUMBER OF SELUK DATE: 1999-10-29
SOFTWAR: PRECENTIN VEX. 2.0
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APPLICANT BARNINGN:
PRINTINGN FURITIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND
TITLE OF INVENTION: PRINTINGN SAME
STILS FRENCHE: ALCOHOLO SOLING SAME
FILE SERENCE: ALCOHOLO POCHEC NO. 6355766 1242-11/2
CORREENT PLIANCIATION UNBER: 05/09/430.503
INVERSE OF DAME: 1299-10.29
SOFFWARS: REMEIR DAME: 1299-10.29
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1 Similarity 21.0%; Pred. No. 4.1e-66;
51; Conservative 32; Mismacches 81; Indels 56; Gaps
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Patent No. 6355786
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Matches 51, Conservative
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            PRIOR APPLICATION NUMBER: 60/091978
PRACR FLIME DATE: 1.998-07-07
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; Patent No. 6355786
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APPLICANT OF THROWN OF THE OWN ISOLATED PROTEIN FERO RELATED (PZR) AND TITLE OF INVESTOR PREPARED AND SCREENING WINNERSON PREPARED AND SCREENING METHODS USING SAME TITLE OF PREPARED AFFORMED AND SCREENING METHODS USING SAME CHEEREN FRILE WEREARD AFFORMED AFFORMED AFFORMED AND SCREENING METHOD AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFORMED AFFOR
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Parent No. 6355786

GREEAL INFORMATION:

TITLE OF INVENTION: PRIFICIAL AND SCREENING MENOR RELATED (2ZR) AND TITLE OF INVENTION: PRIFICIAL AND SCREENING METHODS USING SAME TITLE OF INVENTION: PRIFICATION OF STATEMENTION: OF SAPERING METHODS USING SAME CURRENT PAILOR OF METHODS USING SAME CURRENT PAILOR OF METHOD SAPE 1999-10-29

CURRENT FILMS REG IN NOS: 49

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Best Local Similarity 26.0%; Pred. No. 7.3e-06;
Matches 47; Conservative 21; Mismatches 73;
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; Patent No. 6355786
141 IPLRVTEEAGEDFTSVVSE-
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US-09-430-503-48
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US-09-430-503-42
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EVES--PFQGRLOWNGSKDLODVSITVLNVTLNDSGLYTCNVSREFEREAHRPFVKTTRL 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27 VEVPSETEAVQGNPMKLRCISCMKREEVBAT---TVVEWFYRPEGGKDFL-IYEYRNGHQ 82
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APPLICANT: Also, Existenses
TITLE OF INVENTION: PURIFIED AND ISOLATED PROTEIN ZERO RELATED (PZR.) AND
TITLE OF INVENTION: PURIFIED AND SCREENING METHODS ISING SAME
FILE REFERENCE. ALCOPATO POCKER NO. 6355786 1242-11/2
CURRENY FILLICATION NAMBER: US/09/430, 503
NUMBER OF SEQ 1D NOS: 49
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Score 129; DB 4; Length 199; I Similarity 56.0%; Precal No. 446-06; 446-06; A77; Conservative 21; Mismatches 73; Indels 477; Conservative 72; Mismatches 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Indels 478; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; Conservative 73; 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Patent No. 6355786
GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Sequence 8, Application US/09430503
Patent No. 6355786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 23.0*
Matches 51, Conservative
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SEQ ID NO 8
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TYPE: PRT
CRGANISM: Homo sapiens
US-09-430-503-8
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27 VEVPSETEAVQGNPMKLRCISCMKREEVEAT --- TVVEWFYRPEGGKDFL-IYEYRNGHQ 82

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US-09-430-503-18	Query Match Dasty Match 11.31, Score 17.1 DB 4; Length 209; Bast Local Similarity 26.04; Pred No. 7, 8e-06; Matches 47; Conservative 21; Missacches 73; Indels 40; Gaps 7;	Qy 27 VEVPSETEANQANPMICARCISCHKREBVEATTVVEMPYREBGGKDFL-IYEYRACHO 82	Oy 83 EVESPPCGRLQPNGIXVLAVTLANDGLYTCAVSREEFEBARRPFWKTTRL 140 Db 96 YLGHYPFFYGRIGMAGDLANGLARINERMORTHGTYTCDVGA139	Cy 141 IALRYTERAGEDFTSV9EIMPYILLVFLIALLIEMIXCYRKV9RA 187 Db 140 -PPDIVQPGHIRLYVPRKNLPVPPWWVVGLYTAVLGLLIALLIANLIARRORSKR 198	Qy 188 E 188	Db 199 D 199	RESULT 11 US-09-430-503-20 ; Sequence 20, Application US/09430503 ; Patent No. 635786	1 GARRATION TO THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF THE TRANSPORT OF T	i stue mermander Aucoring Docker No. 6459/86 1242-11/2 ; CURRENT APPLICATION NUMBER: US/09/430, 503 ; CURRENT FILING DATE: 1999-10-29	; NUMBER OF EXPLINOS: 49 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ IN NO 20) TYPER: RRT ; ORGANISM: Room sapiens US-09-430-503-20	Onery Match Beat Local Similarity 26.09; Pred. No. 78-09; Beat Local Similarity 26.09; Pred. No. 78-09; Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;	Oy 27 VEWPSETBANDGANEMILACISCOMCREEVBATTVVEMPYRPEDGANDFL-IYDEYRAGHO 82 Db 40 VYTEKRIFVANGTOGALIA: FISTSTITGALISVSHSEPDEGADDFASTSTITGALIANSTOGATS Db 40 VYTEKRIFVANGTOGALIA: A STATEMENT A STATEME	QY 83 EVBSPPGGRLQMNGSKDLQDVSITVLANVTLANDSGLYTCAVVSREPEFERAHRPFVKTTRL 140		OY 141 IPLATEREDEDFSUVSEIDMYILUMPITIMALIEMIYCYRKYSKA 187	Qy 188 Z 188	Db 199 b 199	RESULT 12 US-09-403-503-22 ; Sequence 22, Application US/09430503	FATER NO. 6259786 ; GREEAL INCOMPATION: ; APPLICART: AMBO, EXITATION: PURITIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND ; TITLE OF INVESTION: PURITIED AND ISOLATED PROTEIN ZERO RELATED (PZR) AND	TITLE OF INVESTIGN: THERAPERITY AND SCHEENING WITHOUS USING SAME: FILE REPRENCY. Attorney Docket No. 6355786 1242-11/2 CURRENT APPLICATION NUMBER: US/09/410,503
Db 40 VYTPKEIPVANGTQGKGTCKFKSTSTTGGLTSVSRASPQPRGADTTVSFPHYSOGOV 95	OY 83 EVESPROCREQUAGSKOLODVSITVLANTLANGGLITTCANGREFEFFEREPEWRITHE 140 Db 96 YLGAYPERORAGOLOFFICH			RESULT 9 - 130-2-430-503-46	; Sequence 46, Application US/09430503 ; Patent No. 6355786	; GENERAL INFORMATION: ; APPLICANT: Zhao, Zhizhuang	TITLE OF INVENTION: PURTIED AND INCIDENT RELATED REPRETIVE CREATER OF THIS OF INVENTION: THEREAPENTIC AND SCREENING WATHOOD USING SAME 1 FILE REPRESENCE: ALCOMAN DOCKER No. 6355796 1242-11/2 CURRENT APPLIANCE DATE: 1999-10-29 1 WINNERS OF SECUL IN MASS. 48	SOFTAMEN SOF	; ORGANISM: Homo sapiens . US-09-430-503-46	Query Match 11.31, Score 127, DB 4; Length 199; Base Local Similarity 26.01; Pecel No. 71.2-06; Matches 47; Conservative 21; Mismatches 73; Indels 40; Gaps 7;	OY 27 VEVPSETBAVOGNEMALACISCHKREBYEATTVVEMFYREPRGAKOFL-IYETRINGHO 82 Db 40 VYTFKIEVVANGTOGALACKRESTSFTOGALSVSNSKOPESADTYTSFFHSQOOP 95	Oy 83 EVESPROCELÇINGSKOLODVSITVLANTIANDSGLYTCKVISREPERAIRPEVUTTEL 140 Db 96 VLANTEKRALSANGOLOKONASIJAIRBNOFINGTYLCTVKRA	YRKVSKA		bb 199 b 199	RESULT 10 US-09-430-503-18	; Sequence 18, Application US/09430503 ; Patent No. 6355786	; GENERAL INPORMATION: ; APPLICANT: Enhang; TILLE OF INVENTION: PRESENCE PROFEIN ZERO PHIAMED PARM	TITLE OF PURENTON THEREABERING AND SCREENING METHODS USING SAME FILE REPRESENCE: ALCORDAY DOCKEN NO. 6355786 1242-11/2 CURRENT PELING DATE: 1999-10-29 ; CURRENT FILING DATE: 1999-10-29	NUMBER OF SEQ ID NOS, 49 SOFTWARE: Patentin Ver. 2.0 ESC ID NO. 1	7 TYPE: RRCJ 7 ONGANIEM: Homo sepiems

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83 EVES--PFQGRLQWNGSKDLQDVSITVLNVTLNDSGLYTCNVSREFEFERHRPFVKTTRL 140
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CURRENT PILLORION UNDERS: US/09/4100,503
UNDERST FILLORION DATE: 1999-10-29
WOMER FILLOR DATE: OF SEQ 1D NOS: 49
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26.0%; Pred. No. 7.8e-06;
tive 21; Mismatches 73; Indels
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ilarity 26.0%; Pred. No. 7.8e-06;
Conservative 21; Mismatches 73;
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Patent No. 6355786
GENERAL INFORMATION:
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US-09-430-503-26
: Sequence 26, Application US/09430503
CURRENT FILLING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
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US-09-430-503-22
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Best Local Similarity
Matches 47; Conserva
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                                                        SEQ ID NO 22
LENGTH: 209
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LENGTH: 209
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SOUTHARN FILLIARD MOTES: 1999-10-29
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iive 23; Mismatches 78
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Search completed: December 5, 2003, 23:24:06 Job time : 31 secs

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OM protein - protein search, using sw model

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1124 1 MPAFNRI.FPLASLVLIYMVS......SDYLAIPSBNKENSAVPVEE 215 US-09-936-680-2 Title: Perfect score: Sequence:

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684280 Total number of hits satisfying chosen parameters: 684280 seqs, 185983659 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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tive 0; Mismatches 4;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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Pagent No. 1050020113203A.

Pagent No. 1050020113203A.

APPLICANT COMPATION: Charles University Technical Services
TITLE OF INVENTION: A novel, family of beta sub-unit proteins from a voltage gated soci
TITLE OF INVENTION: A novel, family of beta sub-unit proteins from a voltage gated soci
TITLE OF INVENTION: Londisc caids encoding them and therapeutic or diagnostic uses to TREAR PERENTION: NUMBER: 12002-04-05
CURRENT PLILAR DATE: 2002-04-05
PRING PAILING DATE: 2002-04-05
PRING PAILING DATE: COT/RECO/1733
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APPLICANT OLITIS (NO.77.A.) SODIUM CHANNEL BETA 4 SUBUNIT,
ITIE OF INVENTION: NO. 10 USES THEREOR
FILE REPERENCE: WILLOUGHER US/10/142, 2018
CURRENT PRILIACYTON UNDERSET US/10/142, 2018
CURRENT PELING DATE: 2002-06-09
PRIAC RELING DATE: 2001-06-19
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
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; Sequence 11, Application US/10142201B
; Publication No. US20030022205A1
; GENERAL INFORMATION:
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SEQ ID NO 1
LENGTH: 215
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ORGANISM: Homo sapiens
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j ORGANISM: Rat
US-09-997-579-1
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Sequence 27, Application 18/09997579

Patent No. USZÓNGD12203AL

GRENERAL INFORMATION:
APPLICANT: CAMPAIGNE University Technical Services

TITLE OF INVENTION: Anomal family of beta sub-unit proteins from a voltage gated so TITLE OF INVENTION: Anomal canida encoding them and therapeutic or diagnostic uses TITLE OF INVENTION: Chalcate caids encoding them and therapeutic or diagnostic uses FILES REFERENCE: 54558-2601

CURRENT PAILNE ON THE . 2002-04-26

CURRENT FILING DATE: 2003-02-24

FRIOR PAILNE DATE: 2003-02-24

FRIOR PAILNE DATE: 2003-02-24

FRIOR PAILNE DATE: 2003-02-24

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100.0%; Pred. No. 2.5e-80;
trive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 159; Conservative
                                                                            205 NKENSAVPVER 215
                                                                                                                                      181 NKENSVVPVEE 191
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: NOVIL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBDNIT
TITLE OF INVENTION: NOVIL GENE
FILE BEPERANCE: 2014.0002/SUB
FILE BEPERANCE: 2014.0002/SUB
FILE SPERENCE: 2014.0002/SUB
FILE STATE FILING DATE: 2000-12-20
FRIOR APPLIANCING NUMBER: US 661,978
FRIOR APPLIANCING NUMBER: US 60/134,198
FRIOR APPLIANCING NUMBER: US 60/134,198
FRIOR FILING DATE: 1999-66-14
NUMBER OF SEQ ID NOS: 23
SOGFWARE: PARENCING NUMBER: US 60/134,198
SEQ ID NOS: 21
LENGAL 1394
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TITLE OF INVENTION: SHEEP, A SOULUM CHANNEL BETA 4 SUBURIT, TITLE OF INVENTION: AND USES THEREFOR CURBER THEREFOR CURBER APPLICATION WINDER: US/10/142, 2018
CURRENT APPLICATION WINDER: US/10/142, 2018
PRIOR FILING DATE: 2001-05-39
PRIOR FILING DATE: 2001-05-39
SOUPHWARE TRANSO OF WINDOWS VERSION 4.0
SOUPHWARE PRESENT OF WINDOWS VERSION 4.0
LENGTH; 215
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Pred. No. 3.4e-95;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1105; DB 15;
Pred. No. 1.3e-107;
0; Mismatches 4;
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Publication No. US20020160453A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.1%;
Matches 211, Conservative
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Best Local Similarity 99.0%;
Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Rattus norvegicus
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ORGANISM: Rattus sp.
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US-10-029-191-4
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Sequence 41, Application US/09997579

Sequence 41, Application US/09997579

Sequence 41, Application US/09997579

SECTION OF THE PROPERTOR: Cambridge University Technical Services and Enablity of Deta sub-unit proteins from a voltage gated so TITLE OF INVESTIGN: Cambridge University Technical Services trins of PROPERTOR: Amovel Seally of Deta sub-unit proteins from a voltage gated so TITLE OF INVESTIGN: Cambridge UNIVESTIGN: Cambridge U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 BEFVKILRYENBVLQLEEDBRFEGRVVWNGSRGTKDLQDLSIFITNVTYNHSGDYQCHVY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 REFEFEAHRPFVKTTRLIPLRVTEEAGEDFTSVVSEIMMYILLVFLTLWLLIEMIYCYRK 183
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                                                                                                                                                                                                                                                                                                                                               10 LASLVLIYMVSVCFPVCVEVPSETEAVQGNPMKLRCISCMKREEVEATTVVEWFYRPEGG 69
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                                                                                                                                                                                                                                                                                                                                                                                                                       S LAPVYGAALVSSAWGGCVBVDSETBAVYGWTPKILCISCKRRSBTTABTFTEWTPROKGT 64
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                                                                                                            Query Match 42.4%; Score 477; DB 14; Length 218; Best Local Similarity 49.5%; Pred. No. 6.8e-72; Marches 106; Conservative 32; Mismatches 68; Indels Matches 106; Conservative 32; Mismatches 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 VSKA-BERAQENASDYLAIPSENKEN-SAVPVEE 215
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SEQ ID NO 44
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Best Local Similarity
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ORGANISM: Rat
         US-10-029-191-20
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US-10-142-201B-8
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Publication No. US/20020160453A1
APPLICAMY: CHRIS, SOYA, J.
APPLICAMY: CHRIS, SOYA, J.
APPLICAMY: CHRIS, SOYA, J.
APPLICAMY: CHRIS, SOYA, J.
APPLICAMY: CHRIS, SOYA, J.
TILE OF INVENTIONS: NOVEL GENE ENCODING A SOUTH CHANNEL BETA-3 SUBUNIT
TILE OF INVENTIONS: NOVEL GENE ENCODING A SOUTH CHANNEL BETA-3 SUBUNIT
TILES OF STREET TO SOUTH CHANNEL SOYA, J. SOUTH CHRIST, J. SOUTH CHANNEL SOYA, J. SOUTH CHRIST, J. SOUTH CHANNEL SOYA, J. SOUTH CHANNEL ELLING DATE: J. SOUTH CHANNEL SOYA, J. SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHANNEL SOUTH CHAN
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Sequence 20, Application US/10029191

GENERAL HIPORANTION: CONTENT S. ROY A.J.

TITLE OF INVENTION: ROYEL SERVE A.J.

TITLE OF INVENTION: ROYEL SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE SERVE
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Pred. No. 3.6e-79;
0; Mismatches 2; Indels
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98.78;
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SOFTWARE: PatentIn Ver. 2.1
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
                                                               157; Conservative
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Best Local Similarity
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Matches 157; Conserv
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ORGANISM: Rattus sp.
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Search completed: December 5, 2003, 23:25:36 Job time : 79 secs
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                               APPLICANT. OUTLIS, PROPY A.J.
TITLE OF INVENTION: 93359, A. SODUTH CHANNEL BETA 4 SUBUNIT, TITLE OF UNEWRITON: AND USES THERROR.
FILE REPRESENCE: HOITOOL.106 FIRMIN)
CURRENT PARILOYNOU MORBER: US; 10/10/142, 2018
FILE REPLICATION WHORER: US; 10/10/142, 2018
FILE REPLICATION WHORER: US; 60/289, 893
FILE RILING DATE: 2001-05-09
FILE RILING DATE: 3001-05-09
FILE RI
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41.9%; Score 471; DB 15;
Best Local Similarity 49.5%; Pred. No. 3.7e-41;
Best Local Sidilarity 49.5%; Pred. No. 3.7e-41;
Best Local Sidilarity 49.5%; Pred. No. 3.7e-41;
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APPLICANT: Millennium Pharmaceuticals Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo Sapiens
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ORGANISM: Rattus sp.
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LENGTH: 218
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GENERAL, INCOMPATION:
APPLICANT: O'GA, ELBA
APPLICANT: O'GA, ELBA
APPLICANT: O'GA, ELBA
APPLICANT: O'GA, ELBA
APPLICANT: D'ANDER, MICHAEL
TITLE OF INVENTION: D'ANDER CHOOLING human betala sodium channel subunit
FILE REFERENCE: ORT. 1221
GENERAL APPLICATION NOMER: US/09/875,456A
WHEREAT FILED D'ANDER: 2001-09-10
APPLICATION NOMER: 2001-09-10
APPLICATION NOMER: ADDIT NOW: 12.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 23.0%; Score 258.5; DB 9
1 Similarity 43.2%; Pred. No. 9.2e-19;
64; Conservative 20; Mismatches 57;
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; Patent No. US20020113203A1
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 64; Conservat
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RESULT 14 US-09-875-456A-14 ; Sequence 14, Application US/09875456A

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GenCore version 5.1.6
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December 5, 2003, 14:16:11; Search time 5264 Seconds Withhour alignments (%) 1999.989 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

UG-09-936-680-4 1261 1 octcocttocgagctgagc......tgccagaactgagaagccgg 1261 Title: Perfect score: Sequence:

2888711 segs, 20454813386 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched: 5777422

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Total number of hits satisfying chosen parameters:

Database :

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ALIGNMENTS

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AB09752.1
AB09752.1
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Oligo capping; fis (full insert sequence)
Macaca facticularia crab-eating macaque)
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Suto,Y., Hital,M., Teraco,K., Suturkl,Y., Sagano,S. and Hashimoto,K.
Assignment of 118 movel. CDNAs of Cynomolygus monkey brain to human
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Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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/clone_lib="macaque_brain_cDNA_library_QmoA"
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LOCUS AXO48005 2612 bp DNA linear PAT 15-DBC-2000 DEFINITION Sequence 2 from Parent WODG69912. ACCESSION AXO48005 10:11876883 KETMOXDS XETMOXDS		REFERENCE 1 AUTHOR Curtis.A. TILL Gene encoding a sodium channel beta-3 subunit protein	Patent: Willenniu	/cognism="Returns app." /col_type="gamonic DNA" DACE COUNT 693 a 655 c 611 g 692 t	tch al Similarity 84.4%;	Matches 655 371	431	133	Db 139 Arcichidakácriokariotariotariokariakákákácakácakácráckáchá 252 Qy 551 TRGFNGAROTTCHAROCCARAGOCCARAGORAKARATHAROTARITHAROTARIAKARA 610	CCTGAG	Db 313 ATGGCCACCAGAAGTGGAGAGCCCCTTCCAAGGCGTCTGCAATGGAATGGAAAGGAAAG 372 Qy 671 ACCTGAGAGGGGGGCGCTTCCATTCCTTAACGTCACTCAGAAGGACTCTCCCCCCAA 730	Db 373 Actrochada Cafratoch Todan Control Articla Trabanda Cafragoch A 132 Oy 731 CTHOLANTOTIC CAGAGATTA ACTT TRAGACACH CAGACACACACC 790	Db 433 CARGGAARGIGTCGAAGAATTCGAAGACACAAGAGCTTTTGTGAAGACAA 492 Qy 791 GACTGATTCACCTAAGAGTCAACAAGAGAGAGAGAGAGACAACACTTTGTGAAGACTTCAAGAGAGAG	Db 493 dactokth.corrisciokstok.cakoideseseseksidadak.cticostoksidesess 552 Oy 851 Aaktohingspokatocakorriscioksesess	TCTTGTTTCTCTCTTGTGTTCTCTTGTGCTCCTAAAAGCCGAAAAAGCCGAAAAAGCCGAAAAAGCCGAAAAAGCCGAAAAAA	613	dy 971 TTGCCATCCCATCTGAGAGGAGAGTCTCGCGTACCGGGAGGGA
CISOMERENEATTWYSMEGGNDELIYEYRKGHOPUSSPPOGELONGSKOLOD VGITULAYTLANGGLYTCHYRRESERBAHEPTWYTTELIPERTERAGEDFSVWSET BASE COUNT 886 a 830 c 659 g 881 c	Ouery Match Bast Local Similarity 66.34; Score 835.8; DB 9; Length 3296; Bast Local Similarity 97.14; Pred 1No. 2:0-197; Indels 4; Gaps 1; Matches 85; Conservative 0; Mismatches 22; Indels 4; Gaps 1;	99 333 AGAAGATCCTCCATCAATAGATTGTTTCCCCTGGCTTCCTCGTCCTTCTTCTCGG 430 Db 1	QV 431 TCACTGCTGCTTCCTGTGTGTGTGAAATGCCCTCGGAAGACGAAACGAACG	99	OV 551 TGSTGANTGGTTCTNCAGGGCGGGGGGGGTTTTTTTCGTATTTTCGTAGTTTCGG 6.10 181 TGSTGANTGGTTCTNCAGGCCGGAGGGCGGGGGTTTTTTTTTT	611 ATGGCCA.CCAGGAGGTGGAGACCCCTTTCAGGGGGCCTGCAGTGGAATGGCAGGAGG 670 241 ATGGCCAGGAGAGAGAGAGCCCTTTCAGGGGGCCTTGAGAGAGG 300	671 ACCISCAGRACOSTOCATCACTOSTOCTCAAACGTCTCTCAACCACTCTCACCA 730 801 ACCTSCAGRACOSTOCATCACTCTCTCAACGACTCTCAACGA 360 802 ACCTSCAGRACOSTOCATCACTCTCAACGACTCTCAACA 360	Oy 731 CCTGCAATGTGTCCCCGGGAGTTTCGAGTTCGAGCCCCTTTGTGAAGACGACCC 790 361 CCTGCAATGTGTCCCGGGGGAGTTTGAGTTCGAGCCCTTTGTGAAGAGGAGCG 220	99 791 GACTGARTCCCCTANAGAGTCACGAGAGACTTCAGACTTCACTCTGTGGTCTCA 850 121 GACTGATCCCACTAAGAGTCACGAGAGAGCGAGAGAGACACTTCACCTCTGTGTCTCA 400	69 851 AAATCATGATGATGATGATGATGATGATGAGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGAGATGA	OY 911 ATTOCTACAGAAAGGTCTCAAAAGCCGAAGGAGGCGCAAGAAAAGGCGTCGACTCACTC	971 TTGCCATCCATCCAAGAACAAGGAAACTCTGCGGTACAAGTGAAGAAAAAGAAA 1030 601 TTGCCATCCAACTGAAACAGAAACTCTGAATCAAGTGAATGAA		Qy 1091 TOANTOGOATCHGARGAGGGCCCCCAAGGGTTCCCTTCATGCATCCATTGTT 1150 Db 721 TOANTOGATCHGARGAGGGCCCCAAGGGTTCCCTTCATGCATCCATT 360	99 1151 CRETCATCATCATCACAAAACAACAACAACAACAAAAAAAAA	1211 CTCCATCAGACCTCTAGGCACATAAGACTGGCAGAACTGAGAGCC 1259	<u>-9</u>

RESULT 6 AX048005

1031 GCAGTGTGACATGAGGTGGCCTGAACACCTGAGGACTGGACATCCCATGTTCAGCAATG 1090

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252 TGGTGGLGTGCTRCAGGCTGAGGGGGGTAAAGATTCCTTATATATGAGTATCGGAGTGCGGGGGGGG	131 CTROAMSTREECONSTREAMST		0y 1001 TOANTOGCARCOLGOAGOGCCCCAAGCCCTCCTTCCTTCTTCTTCTT 840 RESULT 8 ANO47984 AXO47984 13108 bp DNA linear PAT 15-DEC-2000 DETAILTON Sequence 1 from Patent Woodes912. VERTORS AXO47984 AXO47984 CI:11976891 COURT OF AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 BY CI:11976891 COURT OF AXO47984 AXO4798 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO47984 AXO4798 AXO47984 AXO4798 AXO4798 AXO47984 AXO4798 AXO4798 AXO4798 AXO4798 AXO47984 AXO4798 AXO4	REPERBUCE AUTHORS AUTHORS AUTHORS AUTHORS MILEMIN Pharmetoricate, To. FRATURES FRATURES MILEMIN Pharmetoricate, To. FRATURES FRATURES MILEMIN Pharmetoricate, To. FRATURES FRATURES MILEMIN Pharmetoricate, To. MILEMIN Pharmetoricate, T	tch 44.4%; Score 559.6; Similarity 84.4%; Pred. No. 7%; Score 559.6; Conservative 0; Missacches 331 Agadahacchecracharatarrarrarrarrarrarrarrarrarrarrarrarr
Db 727 GTGGTGTGACTGACGACGCCCCAGGGGGCCCCAGTTCACGGTATCCCCAGTTCAGTGATG 785 Oy 1091 TCAATGGCTGACGACGCCCCCAAGGCCCCCTCCTCCTCATCATCATTCAT	WS ESS		source 1.310, 310, 1310,	CIGOMOREANITYUWENTERPOGNOMELTS:TRINGHORDERPOGNALOMORGONOMO	431 TEACHTECTECTECTECTECTES AND TEACTECTECTES AND TEACTES AND TEACHER TO THE TEACHER THE THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE TEACHER THE THE TEACHER THE TEACHER THE TEACHER THE THE TEACHER THE THE TEACHER THE THE TEACHER THE THE TEACHER THE THE TEACHER THE THE TEACHER THE THE THE TEACHER THE THE THE THE TEACHER THE THE THE THE THE THE THE THE THE THE

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131 TCASTGCTGCTTGCTTGGAAGTGCCTCGGAAGTGCGCTGCAGGCCA 490	071 ACCTGOAGAACGTCGTCATCATCTCTCAACGTCATCGTCATCATCATCATCATCATCATCATCATCATCATCATCAT	81 AAATCHTGATGTACTTCTGGTCTTCCTCACCTTGGGCTGCTGATGGGGGGGG	AYC AYC AYC AYC AYC AYC AYC AYC AYC AYC	TITLE A Cheen C. Waters 1 Co. Kazen-Gilleapie, K. and Isom, L.L. TITLE C. Water, C. Kazen-Gilleapie, K. and Isom, L.L. TITLE C. Water, C. Kazen-Gilleapie, K. and Isom, L.L. TITLE C. Massey C. Kazen-Gilleapie, K. and Isom, L.L. JOURNAL Shahtted J. John A. Water, C. Kazen-Gilleapie, K. and Isom, L.L. JOURNAL Shahtted J. John A. Water, M. 48109-0632, USA RSTRIBES III Dev. 6622, Ann Arbor, MI 48109-0632, USA Source /organism="Mus musculus"

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beta 3: an additional auxiliary subunit of the voltage-sensitive sodium channel that modulates channel gating with dissinct kinetics Porco. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Cambridge, Tennis Court Road, Cambridge, CB2 10W, UNITED KINGDOM
Revbised by [3]
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                                                                                                                                                                                                                                                                     Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Jamnock, R.D., Highes, J., Richardson, P.J., Mazuguchi, K. and Jackson, A.P.
                         AJ243395. 2 GI:7242802
scn5b gene, voltage-gated sodium channel beta-3 subunit.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Pred. No. 3.5e-117;
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/mol_type="mRNA"
/db_xref="taxon:10116"
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                                                                                                                            COX.P. Dixon, A. Jackson, A. and Norgan, and Norgan are a voltage-gated sodi the A novel family of beta sub-unit proteins from a voltage-gated sodi un channel, nucled, acids encoding them and therapeutic or patent. We notistate these of Patent. Mo 06537A.A. 2 & CCT-2000, ARMRETAMBERT COMPANY (US), Cambridge University Technical Services Limited (GS)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
Sciurognathi, Suresia, Rodentia, Sciurognathi, Muridae, Murinae,
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/mol_type="genomic DNA"
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RNO241395 22.0 bp mRNA linear ROD 29-JAN-2003 Rattus norvegicus mRNA for voltage-gated sodium channel beta-3 subunit.

LOCUS

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1-15-11 Kitessor, Sugaminara, Kanagawa 228-6555, Japan (8-mill hattorieger, riken, 90-1)p. TML-1htp://hgp.psc.riken.90-jp/, PRL-181-47-79-9934,

On Aug 15, 2000 Hats sequence Version replaced gi:8118870.
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381 CACCTGCAATGTTCCCGGGAGTTTGAGTTTGAGGGCGATCGGCCTTTGTGAAGACGAC 440
                                                                                                                                                                      429 GGTCAGTGTCTGCTTTCCCTGTGTGTGTGTGTGCCCTCGGAGACGGAGACGAGGCCGTGCAGGG 488
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2 Undates 1 to 17.7477 genome, DNA 67 11024.

2 Undates 1 to 17.7477 genome, Taylor, T.D., Hong-Seog, P., Fullattori, M., 18041, T., Toodai, Y., Watcanabe, H. and Sakaki, Y., Direck Submission.
                                                                                                         22 CCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCTGTGCTTATCTACTG 81
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                                                                                 369 CCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTACTG
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Contect: http://kigp.sgc.riken.go.jp
Contect: project name; hmmorthin
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Center close name; Orges-13AL
Sequencing vector; PCR products; 100% of reads
99.5%; Pred. No. 7.1e-91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Advancers of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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2337: gap of unknown length
4912: cante of 2275 be in length
4912: gap of unknown length
4918: gap of unknown length
8889: gap of unknown length
11261: cante of 2575 be in length
11262: gap of unknown length
11263: gap of unknown length
11263: gap of unknown length
16738: gap of unknown length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center clone name: RP11-142P10
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Direct Submission
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                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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HOmo saplens chromosome 3 clone RP11-142P10, WORKING DRAFT
SUSDENCE, 13 unordered pieces.
                             33.9%; Score 42%; DB 2; Length 127347; 100.0%; Pred. No. 1.2e-90; tive 0; Mismatches 0; Indels 0;
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HTG, HTGS PHASE1, HTGS_DRAFT.
HOMO sapiens (human)
HOMO sapiens
                                                Query Match
Best Local Similarity 100.0
Matches 428; Conservative
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50353 CTCCCTTCCGAGGTGAGCTTACCCTGGGCGCAAACGAGGAGGCAGGGCGCGGGAGTGGAA 50294
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                               | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 1980 | 
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38456 a 33920 c 34115 g 37093 t 1249 others
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          contig of 8810
gap of unknown
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
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GenCore version 5.1.6
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December 5, 2003, 14:12:31; Search time 475 Seconds Withbour algomental 7166.298 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

1 ccctcccttccgagctgagc.....tgccagaactgagaagccgg 1261 US-09-936-680-4 Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Searched:

5105512 foral number of hits satisfying chosen parameters: 2552756 segs, 1349719017 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N Geneseq 19Jun03:* Database :

| M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Juliura); | M. Centered, Jennesed, Genereden-embl. MA1981, DMT: | M. Centered, Jennesed, Genereden-embl. MA1981, DMT: | M. Centered, Jennesed, Genereden-embl. MA1981, DMT: | M. Centered, Jennesed, Genereden-embl. MA1981, DMT: | M. Centered, Jennesed, Genereden-embl. MA1981, DMT: | M. Centered, Jennesed, Genereden-embl. MA1981, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centered, Jennesed, Genereden-embl. MA1991, DMT: | M. Centereden-embl. MA1991, DMT: | /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

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Result		Query				
No.	Score	Match	re Match Length DB I	DB	ID	Description
1				į.		
-	1261			5	AAC67837	Human beta3 cDNA.
64	1252.2			24	ABA93727	Human signal trans
m	909,4			22	AAF84146	Human novel sodium
4	871.8			22	AAK52345	Human polynucleoti
ιn	858.6	68.1	978	22	AAH98320	Human EST-derived
9	561.8			53	AAS86764	DNA encoding novel
7	559,6			55	AAC90602	Rat sodium channel
8	559.6			22	AAC90600	Rat sodium channel

	DNA encoding novel DNA encoding novel Human reproductive Human resticutar a Rabbit sodium chan Human voltage-gate	Human voltage-gate Human polymucleoti Rat sequence diffe Human betalA sodiu Human polymucleoti Rat sodium channel Sodium channel	Maine gerandy gerand	Mouse ischeemic co Drocophila melanog Procophila melanog Reacdomonas aerugi Human pol-activate Human pol-activate Human pol-activate Noval human cerino (*hreo Noval human china Drocophila melanog Rocophila melanog Roman i
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110	25 4 5 5 7 5	232129	222222222 20222222242	
		0 0		0 000

ALIGNMENTS

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Human, beta sub-unit; beta; analgest; articonvulsant; cerebroprotective; vacorropic; cardiant; noctropic; cytostatic; dermaclogical; gen tharapy; voltage-state godium channel; pain; esplieps; stroke; stechemia; heart disease; Jacobsen Syndrome; familial nochromefitin paragogilome; pheny disease; Jacobsen Syndrome; Charcot Warie Troke; stechemia; heart disease; Jacobsen Syndrome; Charcot Warie Troke; session; ses.
                                                                                  AAC67837 standard; cDNA, 1261 BP
                                                                                                                                                                                                                                                       15-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                         Human beta3 cDNA.
                                                                                                                                                                    AAC67837;
RESULT 1
                                                AAC67837
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24-FEB-2000; 2000WO-EP01783. 99US-0129473. WO200063367-A1. 15-APR-1999; Homo sapiens. 26-OCT-2000. X8X8X8X8X8X8X8X8X8X8X8X8X8X8X8X8

(WARN) WARNER LAMBERT CO. (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD. Morgan K; Dixon A, Jackson A, Cox P,

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661 GGCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCT 720
                                                                                                                                   721 GGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGTTGAGGGCGCATCGGCCTTTGTG 780
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                              661 GGCAGCAAGGACCTGCAGGACGTGTCCTGTGCTCAACGTCACCTCTGAACGACTCT
                                                                                          GGCCTCTACACCTGCAATGTGTCCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTG
                                                                                                                                                                                    781 AAGACGACGCGGCTGATCCCCCTPAGAGTCACCGAGGAGGAGGAGGAGGACTTCACCTCT
                                                                                                                                                                                                                  Human; foetal brain; foetal kidney; melanoma; testis; amygdala;
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                                                                                      Novel nucleic acids encoding a beta-3 subunit from a voltage-gaved sodium channel, and their corresponding polymeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke -
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                                                                                                                                                                                                                  Claim 10; Page 70-71; 88pp; English.
                                 WPI; 2000-665241/64.
                                                        P-PSDB: AAB36002.
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The present invention describes seesablages and computer readable media compute significant neutral officers. The seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesablage seesabl
                                                                                 Human CDNA sequences and clones derived from human fetal brain, fetal kidney, melanoms, testis and amygdala cDNA libraries, useful in genetic screening and therapy -
                                                                                                                                                                                                                                                                                                                                                                     Claim 1, Page 174-175; 611pp; English.
P-PSDB; ABB05689.
#X####X#X99999999
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Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 other;

70	portenhao		
Query Best L	Match	Query Match 99.3%; Score 1252.2; DB 24; Length 4052; Best Local Similarity 99.8%; Pred, No. 0;	
Matche	9 125	vative	
à	m	CTCCCTTCCGAGCTGAGCTTACCCTGGGCGCAAACGAGCGAG	
qc	431	CICCTICCGAGCIGACTIACCCIGGGCGCAACGAGCGAGGCAGGGGGGGGGG	_
δ	63	GCTGGAGTTCCGGGCTGGCCGGGAGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGC 122	
ą	491	GCTGGAGTTCCGGGGTGGCGGGGGGGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGC 550	_
δ'n	123	GGGCGCGGAGCGCCGCTGATCGCCTCCCTCGAACTGGGGACCCAGTGGGGTCCCTTAGGG 182	
q ₀	551	GGGCGCGGAGCGCCTGATCAGCTCCCTCGAACTGGGGAGCCCAGTGGGGTCGCTTAGGG 610	_
٥٨	183	CCCAAAGCCCCCACCCGGCTCCAAAAGCTCCCAGGCCTCCCCAGGCACGGCACGGTCGC 242	
q	119	CCCAAAGCCCCCGCCCGGCTCCAAAAGCTCCCAAGGCCTCCCCAAGGCGCGCGGTGCTCGGC 670	_
λά	243	CCTTCCTTCGGTCAGAAAGTCGCCCCCTGGGGGCAGTTCGTCCAAAGGTTTCCTCGAA 302	
q	671	CCTTCCTTCGGTCAGAAAGTCGCCCCTGGGGCAGTTCGTCCCCAAAGGGTTTCCTCGAA 730	_
È	303	AGANICYGAGAGGGCGCNGTCCTTGACCGAGGGAAICTCTCTGTGTAGCCTTGGAAGCCG 362	
QQ	731	AGAATCTGAGAGGGGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAAGCCG 790	_
λŏ	363	CCAGCCCCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTAT 422	
qq	791	CCAGCCCCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCTGGTTAT 850	_
οχ	423	CTACTGGGTCAGGTCTGCTTCCCTGTGTGTGTGABAGTGCCCTCGGAGACGGAGGCCGT 482	
qq	851	CTACTGGGTCAGTGTCTTCCCTGTGTGTGGAAGTGCCCTCGGAGACGGAGGCCCT 910	_
κά	483	GCAGGGCAACCCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGAG	
qq	911	GCAGGCCAACCCCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGAG	_
à	543	CACCACGGTGGTAGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGA 602	
qq	971	CACCACGGTGGAATGGTGTACAGGCCCGAGGGGGGTAAAATTTCCTTATTACGA 1030	2
č	603	GTATCGBANTGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGG 662	
q	1031	GTATCGGAATGGCCACCAGGAGGTGGAGGCCCCTTTCAGGGGCGCCTGCAGTGGAATGG 1090	0
δ	663	CAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGG 722	
QQ	1091		0

Novel sub-unit for voltage-gated sodium channel proteins for producing

Sanseau P;

Plumpton M, Powell AJ,

WPI; 2001-398129/42. P-PSDB; AAB85206

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1451 GAACAGGAGCAGTGACATGACATGGCCTCAACACCTGAGGGACTGGACATCCCATGTT 1510
                                                                                                                                                                                                                                                                                                                                                                                                                             1571 CCATTGTTCTGTTCATTCATTCATCCACCACTGCCTCTGAGCTTTCACCTCTGA 1630
             1331 GATGATATTTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGCCCCAAGAAAACGCGTC 1390
                                                                                                                                                                                                                              963 TGACTACCTTGCCATCCCATCTGAGAACAAGAGAACTCTGCGGTACCAGTGGAATA 1022
                                                                                                                                                                                                                                                                                           1082
                                                                                                                                                                                                                                                                                                                                                  1083 CAGCAATGFCAATGGCAFCAGGAGGCGCCCCAAGGGCCCCATCGCTTCCCTTCATGCAT 1142
                                                                                                                                                                                                                                                                                                                                                                     1143 CCATTGITCTGITCATTCATCCACATACATCCACCTGCCTCTGAGCTTTCACCTCTGA 1202
                                                                                 1211 GACGACGCGCCTGATCCCCCTAAGAGTCACCGAGGAGGCTGGAGGAGGACTTCACCTCTGT 1270
                                                                                                                                                                       962
                                                                                                                                                                                                                                                          1391 TOACTACCTTGCCATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGAATA 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1203 CTCCCTAACTCCATCAGACCTCTACGCACCATAAGACTCTGCCCAGAACTGGGAAGCC 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1631 CTCCCTAACTCCATCAGACCTCTACGCACATAAGACTCTGCCAGAACTGAGAAGCC 1687
CCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAA
                                                     783 GACGACCGCCTAAGAGTCACCCCTAAGAGTCACCGAGGAGGAGGAGGACTTCACCTCTGT
                                                                                                             GGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGA
                                                                                                                                                                         903 GATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCCCCAAGAAAACGCGTC
                                                                                                                                                                                                                                                                                        1023 GAACAGGAGCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sodium channel; sensory neurone specific channel; betal-like subunit; SNS; therapeutic; pain; analgesic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "sodium channel betal-like subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel sodium channel betal-like subunit encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
213..860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAF84146 standard; cDNA; 1510 BP
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1189 GCTTTCACCTCTGACTCCCTAACTCCATCAGACCTCTACGCACCATAAGACTCTGCAGA 1248
                              The invention values to polyunalcules (DANSISA AAKSIS) and the concided pulsages AAKSISA) and the concided pulsage the polymential of the satishir activity abiting to cytochine of proliferentiation or which may induce production of other optoximas in other cell populations. The polymucleotides and polypeptides are useful in deser bareay. Waccines or peptide thereay. The polypeptides have various cytokine-like activities, e.g. seem cell growth factor activity, heasaropolesis regulating activity, tissue growth factor activity, immunomodulatory activity and extinifyinhis activity and may be useful in the diagnosis and/or regeneral concerns a property factor activity increases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, cytokine; cell proliferation; cell differentiation; gene therapy; veccine; pepticle thrapy; stem cell growth factor; hadmatopolesis; inminomodilatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: RECORDS for SEQ ID NO 2110 (AAKS2SB1), 2111 (AAKS2SB2) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cac Y, Wang D, Wang Y, Zhang Y, Ren F, Chen R, Wang ZH, Weihrman T, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 2934-2935; 6221pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                             Auman polynucleotide SEQ 1D NO 890.
                                                                                                                                                                                                                                                                        AAK52345 standard; cDNA; 1045 BP.
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15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
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                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001 (first entry)
                                                                                                         ACTGAGAAGCC 1259
                                                                                                                                                       1086 ACTGAGAAGCC 1096
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                                                                                                                                                                                                                                                                                                                          AAK52345;
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                                                                               The invention provides a novel beat-like sub-unit for voltage-gated codium ion channal polyperide, pecifically a sensory neurone specific channel (885) subunit. The novel betal-like subunit is useful for channel (885) subunit. The novel betal-like subunit is useful for setting to producing a theorepactic organic which is useful in a patient. The subunit can be expressed by standard accombinant methodology. The present sequence represents a human novel sodium channel betal-like subunit emodaing cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>GRGRCGGRGGCCGFGCCAGGCCAACCCCATGAAGCTGCGCTGCATCFCCTGCATGAAGAGA</u>
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                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                      DB 22, Length 1510,
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                                                                                                                                                                                                                                                                        Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 other;
                                                                                                                                                                                                                                                                                                                          Score 909.4; DB 22;
Pred. No. 2.5e-234;
0; Mismatches 1;
                                             Claim 4; Page 29-30; 31pp; English.
agents useful for treating pain
                                                                                                                                                                                                                                                                                                                          72.1%;
                                                                                                                                                                                                                                                                                                                                                                       Matches 910; Conservative
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Human BST-derived coding sequence SEQ ID NO: 177.

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                                                                                                                                                                                                                                                                                      192 CCCCTGGGGGGCAGTTCGTCCAAAGGGTTTCCTCGAAAGAATCTGAGAGGGCGCAGTCCT 251
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                                                                                                                                                                   TCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTACTGGGTCAGTGTCTGCTTCC 445
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                                                                                                                                   CCCTCGAACTGGGGAGGTCCAGTGGGTCGCTTAGGGCCCAAAGCCCCCACCCGGCTCCA
                                                                                                   12 GTGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGCTGGCGCGGGAGCGGGTGATCGGCT
                                  0; Gaps
Score 871.8; DB 22; Length 1045;
Fred. No. 2.8e-224;
0; Mismatches 7; Indels 0;
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  Query Match 69.1%;
Best Local Similarity 99.2%;
Matches 876; Conservative
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proceins from a variety of organisms, including human, dog, cat, horse, cow, pig, handrer, mondey, madeaque, yeast, bacteria, fruit fly, sea urchin and constor. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in disgnostice, for forcemize, gene mapping, identification of muttation, to assesse biodiversity and for mutritional purposes. The present sequence is a cDNA biodiversity and for mutritional purposes.
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L155 AAAGCTCCCAGGGCCGGCAGCAGCGGTCTCGGCTCGGTCAGAAAGTCGC 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 GAGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGCGGGCGCGGAGCGGCTGATCGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                        Human; sheep; pig, cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea trichin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping genetic disorder; blockyvestly; gene thetapy; nutrition; se.
                                                                                                                                                                                                                                                                                                                                                                            Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.1%; Score 858.6; DB 22; Length 96.2%; Pred. No. 9.7e-221; ive 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 978 BP; 193 A; 283 C; 293 G; 209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Zhou P, Qian XB, Wang Z,
Cao Y, Drmanac RA, Zhang J, Werhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 299-300; 1275pp; English.
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03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
                                                                                                                                                                                                                     25-JAN-2001; 2001WO-US02687.
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446 CTGTGTGTGTGGAAGTGCCCTCGGAGACGGAGGCCGTGCAGGGAACCCCATGAAGCTGC 505

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12-OCT-2001 (first entry)

AAH98320;

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976 CTTGTGGCTGCTCATCGAGATATATTGCTGAGACAGGTCTCAAAAGCCGAAGAGGC 1035
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CIGTGTGTGTGTGTGGAGTGCCCTCGGAGACGGTGCAGGGCAGCACCCCATGAAGCTGC 424
                                         GCTGCATCTCCTGCATGAAGAGAGAGAGGTGGAGGCCACCACGGTGGTGGAATGGTTCT 565
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                                                                                           56 ACAGGCCCGAGGCCGTAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACCAGGAGG 625
                                                                                                                 485 ACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACCAGGAGG 544
                                                                                                                                                                     545 TGGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGGACCTGCAGGACGTGT 604
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                                                       605 CCATCACTGTGCTCAACGTCACGTCTGAACGACTCTGGGCTCTACACCTGGGAATGTGTCCC
                                                                                                                                          TOGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTGCAGGACGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG22577.
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responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                                                                                                                                            Claim 1; SEQ ID No 22568; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             727 GRGGIGIGACITGAGGIGATCIG-AGIGCIGAGGGACIGGAIAICCCCAGIICAGIGAIG 785
313 ATGGCCACCAGGAAGTGGAGAGCCCCTTCCAAGGCCGTCTGCAGTGGAATGGGAGCAAAG 372
                                               671 ACCTIGCAGGACGTGTCCATCACTGTGCACTCTCTGAACGACTCTGGGCCTCTACA 730
                                                                                                                                              CCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGCGCCATCGGCCCTTTGTGAAGACGACGC 790
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                                                                                                                                                                                                                                                                                            493 GACTGATACCTTFGCGAGTCACTGAAGAGGCGGGAGAAGACTTCACCFCCGTGGTCTCGG 552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 AAATCATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCGAGATGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 AAAAGATGCCTGCCTTCAACAGATTGCTTCCCCTAGCTTCTCTAGTGCTCATCTACTGGG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGTGTCTGCTTCCCTGTGTGTGTGTAAGTGCCCTCGGAGACGGAGGCCGTGCAGGGCA 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGA 610
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                                                                                                                                                                                                                                                                                                                                Rat sodium channel beta3 protein Alrxa94h5 related seguence.
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Best Local Similarity 84.4%; Score 559.6; DB 22; Length
Best Local Similarity 84.4%; Pred. No 3.9e-140;
Matches 655; Conservative 0; Mismatches 114; Indele
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                                           1036 AGCCCAAGAAACGCGCCAGGAAC 1060
               945 AGCCCAAGAAACGCGTCTGACTAC 969
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                                                                                                                                                                                 AAC90602 standard; DNA; 2632 BP.
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                                                                                                                                  RESULT 7
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Rat beta3 subunit cDNA.

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involved in the generation of pain and other sensory or perceptive nerve impulses, in the establishment and endurance of mood, neurodepenerative and stabep disorders, and in the control of muscle contraction, including movements such as the heartbear, dispection and vascular cone. The sequences can be used in predictive medicitie, screening and diagnostic.
                                                                                                                                                                                                                                                                                                        assays, and in pharmacogenomics.
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Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 other;

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TIBCCATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAATAGAACAGGA 1030
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                                                                                                                                                                                                           371 AGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTACTGGG
                                                                                                                                                                                                                                             AAAAGATGCCTGCCTTCAACAGATTGCTTCCCCTAGCTTCTCTAGTGCTCATCTACTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 613 ATTGCTACAGAAAGGTCTCTAAGGCCGAAGAGGCACCACAGGAAAATGCGTCTGACTACC
                                                                                                                                                                                                                                                                            TCAGTGTGTTCCCTGTGTGTGTGTGTGTGTGCCCTCGAAGAGGGAGAGAGGCCGTGCAGGGCA
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                                                                                                                                            DB 22; Length 3108;
                                                                                                                                                                            Indels
                                                                                                                                          Score 559.6; DB 22;
Pred, No. 4.2e-140;
0; Mismatches 114;
                                                                                                                                          Query Match
Best Local Similarity 84.4%;
Matches 655; Conservative
                                                                                                                                                                                                                                                                                                                                           491
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AAC67836 standard; cDNA; 2220 BP
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGGAATGGTTCTACAGGCCCGAGGCGGTAAAGATTTCCTTATTTACGAGTATCGGA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538 TGGTGGAGTGGFTCTACAGGCCTGAGGGCGGTAAAGATTTCCTTATATGAGTATCGGA 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 ATGGCCACCAGGAAGTGGAGAGCCCCTTCCAAGGCCGTCTGCAGTGGGAATGGGAAGGCAAAG 657
                                                                                            Rat; beta sub-unit; beta3; analgesic; anticonvulsant; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present exquence is given in the clime of a specification relating to a novel family of beta sub-unit proteins from a voltage of a columnic. Hamma and rate best sub-units, which have been collectively identified as beta; have been isolated in the polymeclectides and polypeptides are useful for screening for agonists and antagonists of sodium channels. The agonists, autagonists or conditions associated with voltage-gated sodium channels, e.g. pain, spinghow, estroke, isohameia, heart disease, accobase systomes, familial Nondramaffin Paragnafilma, Phenylecomita and Charcom, Familial Nondramaffin Paragnafilma, Phenylecomita and Charcom Familial Nondramaffin Paragnafilma, Phenylecomita and Charcom Familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for selecting and treating sodium channel-associated conditions, e.g., pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AGAAGAFGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTAGTGGG
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                                                                                                                             vasotropic, cardiant, nootropic, cytostatic, dermatological; gane therapy, voltage-gated sodium channel, pain, epilepsy; stroke; tennista nonthrometiff naveadosen Syndrome; tennista nonthrometiff naveadosen Syndrome; contrain, channel, contrain, channel, sodium channel, see contrain contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see contrains, channel, see c
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Pred. No. 6.9e-135,
0, Mismatches 70, Indels 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WARN ) WARNER LAMBERT CO.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morgan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 69-70; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dixon A, Jackson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2000; 2000WO-EP01783.
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Matches 582; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epilepsy and stroke -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-665241/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-APR-1999;
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                                                                                                                                                                                                                                                                                                                                             Rattus sp.
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0; Gaps

0; Mismatches 69; Indels

Matches 576; Conservative

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                                                                                                                                                                                                                                                                                911 NITGCTACAGNAAGGTCTCAAAAGCCGAAGAGCGAGGCAAGAAAACGCGTCTGACTACC 970
                                                                                                                                                                                                                                                                                                                 957
                                                                                                                                                                         778 GACTGATACCTTTGCGAGTCACTGAAGAGCGGGGAGAGACTTCACCTCCGTGGTCTCGG 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invertion provides the protein and coding sequences of the ret codium channel beta protein; designated Alras94fb. This protein is livolved in the generation of pain and other sensory or perceptive nerve famplises. An the sexabilisement and enformation of mod, neurodesenseative and steep disorders, and in the control of mascle contraction, including movements such as the beartheart, delegation and vascular comes. The sequences can be used in predictive medicine, sorteening and diagnostic
                                                                        CCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGC
                                                                                                                                                                                                                                                                                                         898 ATTGCTACAGAAAGTCTCTAAGGCCGAAGAGGCAGCACAGGAAAAAGGCGTCTGACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
root ganglion cDNA library for use in obrenseome mapping, forenalc
medicine, monitoring clinical trials and therapeutics
                                                                                                   718 CATGCAATGTGTCCAGGGGTTCCAATTCCAGGCACACAGGCCTTTTGTGAAGACCACGA
                                                                                                                                          GGCTGATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGCTCTCAG
                                                                                                                                                                                                             AAATCATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAGATGATAT
                                                                                                                                                                                                                                            838 AAATCATGATGTACATCCTCCTGGTCTTCCTCACCTTGTGGCTGTTTATTGAGATGATCT
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DB 22; Length 645;

Pred. No. 1.2e-133; 42.4%; Score 534.6;

89.38

Best Local Similarity

Query Match

Sequence 645 BP; 155 A; 154 C; 181 G; 155 T; 0 other;

assays, and in pharmacogenomics.

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195
376 ATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCGTGCTTATCTACTGGGTCAGT 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602 AGINICOGRATGOCCACCAGAGAGGTGAAQAGCCCCTTTCAGGGGGGCGCTGCAGTGAANG 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   422 TCTACTGGGTCAGTGTCTGCTTCCCTGTGTGTGGAAGTGCCCTCGGAGACGGAGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542 CCACCACGGTGGTGGAATGGTTCTACAGGCCGAGGGCGGTAAAGATTTCCTTATTTACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                    Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated polymucleotide and encoded polypeptides, useful in diagnostics, formstice, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 3531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3531 BP; 952 A; 901 C; 960 G; 718 T; 0 other;
                    DNA encoding novel human diagnostic protein #22567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 3.7e-95;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 392.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 22567; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.1%;
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                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 395; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ABG22576.
                                                                                                                                                                                                 MO200175067-A2.
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity
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                                                                                                                                                                                                                                                                              This sequence represents an expressed sequence tag (EST), and is a polymolecetise of the invention. The polymolecetise of the invention. The polymolecetise of the invention are all secretaed EST sequences isolated from a variety of human tissue the sequences isolated from a variety of human tissue reserved. The sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence is the sequence in the sequence is the sequence are also stated to be useful for gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 CCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGGTGCTTATCTACTG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       429 GSTCAGTGTCTGCTTCCCTGTGTGTGTGGAAGTGCCCTCGGAGACGGAGGCCGTGCAGGG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 GGTCAGTGTCTGCTTCCCTGTGTGTGTGTGCCCTCGGAGACGGA-GCCGTGCANGG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489 CAACCCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGAAGAAGGAGGAGGCCACCAC 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 GGTGGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTAGGAGTATCG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATGGCCACCAGGAGGGGGGGCCCTTTCAGGGGGGGCCTGCAGTGGAATGGCAGCAA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261 GNATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCTGCAGTGGAATGGCAGGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTA 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACCIGCAARGIGICCCGGGGAGIIIGAAGAGGCGCCAICGGCCCIIIGAAGACGAC 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               381 CACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGGCGCATCGGCCCTTTGTGAAGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 CCRGARGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTACTG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                                                                                                                             New polynucleotides encoding human secreted proteins - derived from
                                                                                                                                                                     e.g. human blood, kidney, foetal lung, placenta, testes, brain, ovary, pituitary, retina and colon cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 429; DB 20; Length 471;
Pred. No. 2.7e-105;
                        Lavallie ER, McCoy JM, Merberg D;
Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                     Claim 1; Page 383-384; 633pp; English.
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                        Agostino MJ, Jacobs K,
Racie LA, Spaulding V,
                                                                                                WPI; 1999-070076/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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AAS86763
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595 ATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCCTGCAG 654
                                                                                                                                                                                                          58 ATTIACGAGIATCGGAATGGCCACCAGGAGGTGGAGGCCCCTTTCAGGGGGCGCCTGCAG 117
                                                                                                                                                                                                                                                                                          118 TGGAATGGCAGCAGCAGCAGGACGTGCCATCACTGTGCTCAACGTCACTCTGAAC
                                                                                                                                                                                                                                                                                                                                     115 GACTCFGGCCTCFACACCFGCAATGFGTCCCGGGAGFTTTGAGGCGCATCGGCCC 774
                                                                                                                                                                                                                                                                                                                                                            178 GACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGGTTGAGGCGCATCGGCCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, reproductive system related antigen, reproductive system disorder;
                                                                                                                                                                                                                                                     655 TGGAATGGCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGTGAAC
                                                                                  17.8%; Score 224.4; DB 23; Length 621; 99.6%; Pred, No. 3.3e-50; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human reproductive system related antigen DNA SEQ ID NO: 7659.
                                                                                                                                                                                                                                                                                                                                                                                                                    775 TITGIGAAGACGACGCGGCTGATCCCCCTAAGAGTCACCGAGGAGG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                           238 TITGTGAAGACGAGCCGGCTGATCCCCCTAAGAGTCACTGAGGAGG 283
                                           Sequence 621 BP; 156 A; 155 C; 175 G; 135 T; 0 other;
at ftp.wipo.int/pub/published_pct_sequences
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2000US-0189874.
2000US-0190076.
2000US-0198123.
                                                                                                      Sest Local Similarity 99.6%;
datches 225; Conservative
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16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
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                                                                                      Query Match
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                                                                                  3191 GCAGCAAGGACCTGCAGGACGTGCCATCACTGTCAACGTCACGTCACTTGAACGACTCTG
                                                                                                                                                     3251 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA 3310
      3131 AGTATCGGAATGGCCACCAGGAGGTGGAGGCCCCTTTCAGGGGCGCGCTGCAGTGGAATG 3190
                                           662 GCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTGAACGACTCTG 721
                                                                                                                          722 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGTGGGCGCATCGGCCCTTTGTGA 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                 3311 AGACGACGCCGGTGATCCCCCTAAGAGTCACCGAGGAGG 3349
                                                                                                                                                                                                             782 AGACGACGCGCCTGATCCCCCTAAGAGTCACCGAGGAGG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #22566.
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                                                                                                                                                                                                                                                                                                                                                         AAS86762 standard; cDNA, 621 BP.
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23-AUG-2000; 2000US-0649167.
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1044 AGGTGGCCTGAACACTGAGGACTGGACATCCCATGTTCAGCAATGTCAATGCCATCAG 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of a number of human reproductive system related missings in these can be used in the prevention and treatment of reproduct hat system disorders, including among the present sequence is a genomic sequence encoding a protein to the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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17.1%; Score 216; DB 22; Length 4625;
Best Local Similarity 100.0%; Pred. No. 1.38-47;
Matches 215; Conservative 0; Mismatches 0; Indels 0.
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                                                                                                     2000US-0249212.
2000US-0249213.
2000US-0249214.
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                                           2000US-0249207.
2000US-0249208.
2000US-0249209.
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2000US-0249211.
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2000US-0256719.
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2000US-0251868
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01-DEC-2000;
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1224 CTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1259

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08-NOV-2000, 200003-0246525.
08-NOV-2000, 200003-0246526.
08-NOV-2000, 200003-0246527.
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2000US-0246532
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    Human; testicular anticul, testes jo cancer; testestasis; immino disorder; recodettive system disorder; training disorder; gene therapy, cardiovarental disorder; gene therapy, acardiovasental disorder; respiratory disorder; marviological disorder; gentroining systemidant disorder; sepiratory disorder; marviological disorder; gentroininestinal disease; infection; cyrocatatic; gene; ds.
                                                                                                                                                      Human testicular antigen encoding DNA fragment SEQ ID NO: 2516.
213 CTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 248
                                                                             ABL97864 standard; DNA; 4625 BP.
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07-707- 2000; 200018- 0205515.
07-707- 2000; 200018- 0205467.
30-707- 2000, 2000018- 021486.
30-707- 2000, 2000018- 021513.5
07-707- 2000, 2000018- 021513.5
07-707- 2000, 2000018- 021513.5
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26.-10.-2000; 2000018-021.295.
26.-10.-2000; 2000018-022096.
14.-N0.-2000; 2000018-022096.
14.-N0.-2000; 2000018-022096.
14.-N0.-2000; 2000018-0228.11.
14.-N0.-2000; 2000018-0228.11.
14.-N0.-2000; 2000018-0228.11.
14.-N0.-2000; 2000018-0228.11.
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14-NG-2000; 2000B-022547
14-NG-2000; 2000B-0225747
14-NG-2000; 2000B-0225758
14-NG-2000; 2000B-022578
18-NG-2000; 2000B-022578
22-NG-2000; 2000B-022578
22-NG-2000; 2000B-022681
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02-WAR-2000; 2000US-0186350.
16-WAR-2000; 2000US-0189874.
17-WAR-2000; 2000US-0190076.
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23-AUG-2000; 2000US-0227009.
30-AUG-2000; 2000US-0228924.
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                                                                                                                              21-JUN-2002 (first entry)
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08-SEP-2000;
08-SEP-2000;
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ABL97864
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1044 AGGIGGCCTGAACACCTGAGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCAG 1103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and colding sequences of 973 human restrictlar antiques, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, repproductive system, immune, respiratory, na marchosgical and agastroinmental disorders, infections, and exticulary cancer, see sepecially restrictlary cancer. The present sequence is a DNA encoding a protein fragment of the invention.
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17-807-2004; 20048-20426.
17-807-2004; 20048-204229.
17-807-2004; 20048-204329.
17-807-2004; 20048-204320.
11-BC-2004; 20048-2016; 20048-2016; 20048-2016; 20048-2016; 20048-2016; 20048-2016; 20048-2016; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2019; 20048-2
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                요
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GenCore version 5.1.6
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December 5, 2003, 17:08:07; Search time 3728 Seconds (without alignments) 8221.015 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

1261 1 ccctcccttccgagctgagc.....tgccagaactgagagccgg 1261 US-09-936-680-4 Perfect score: Sequence: Title:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table;

Searched:

45562784 Total number of hits satisfying chosen parameters: 22781392 segs, 12152238056 residues

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES

Beult Query No. Score Match Length DB ID Description	BX420015 BX420015	BX445002 BX445002	AK076466 Mus muscu	AK049747 Mus muscu
QI	BX420015	BX445002	AK076466	AK049747
80	13	23	1	Ξ
* Query Match Length DB	1201	1201	1359	3549
% Query Match	61.2	51.8	43.7	43.0
Score	771.8	652,6	550.6	542.6
Result No.	-	7	٣	4

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AL IGNMENTS

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BX420015 Good Sapiens FETA 1201 bp mRNA linear EST 13-MAY-2003
BX420015 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone
CSDPF023XA09 5-FRINE, MRNA sequence. Homo arbitems blackround, Craniata, Vertebrata, Eureleostomi, Mourabla, Burberaca, Chordata, Craniata, Vertebrata, Eureleostomi, Mourabla, Burbera, Primates; Catarrhini, Hominidae, Homo. 1 (hease 1, to 1201) 1. (hease 1, to 1201) 1. (hease 1, to 1201) 1. (hease 1, to 1201) 1. (hease 1, to 1201) 1. (hease 1, to 1201) 1. (heaved 1, to 1201) 1. BX420015,1 GI:30646738 Homo sapiens (human) BX420015 VERSION KEYWORDS SOURCE ORGANISM DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS ACCESSION RESULT 1 BX420015

Comparations of the control of Sequencing entering the control of Sequencing entering the control of Sequencing entering the control of Sequencing entering

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ESOBPEGATMOS 5-PELME, MRNA sequence.
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11, Wai. Gruber, C., Jessee, J. and Polayes, D.
12, Wai. Gruber, C., Jessee, J. and Polayes, D.
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Libmary was constructed by Life Technologies, a division of 
Invitrogen. This sequence belongs to sequence cluster 6147.r For 
more Lifermation about this cluster, see
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cgi-bhi/cluster.coj?seq-CSIAF00622000pl.eluster=6147.r. Contact
Feng i.Mang Bakil. Gliangshifetech.com (Wil. :
Feng i.Mang Bakil. Gliangshi.suvitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genocope sequence ID : CSIAF0062E050Pl.
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/mol_type="mRNA"
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/clone="CS0DF023YA09"
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Faraday Avenue Genoscope sequence ID : CSODF023AA05QP1.
Location/Qualifiers
                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                   /db xref="taxon:9606"
/clone="CS0DF023YA09"
                                                                                                                                                      /mol_type="mRNA"
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Best Local Similarity 92,7%
Matches 800, Conservative
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AL Genome Res. 10 (11), 1757-1771 (2000) Reads, J. Shinngawa, R. Shibara, X. Yoshino, M., Itoh, M., Ishii, Y. S. Rawas, J. Shinngawa, R. Shibara, X. Yoshino, M., Itoh, M., Ishii, Y. Alarea, K. Tarasa, M. Whith, K. X. Yosawa, H. Adonii, J. Fibria, S. Alzea, K. Alzea, M. Mishi, K. Yosawa, T. Wannaka, I. Saito, T. Okazaki, Y. Gojobori, T. Bono, H. Kesukawa, T. Saito, R. Radora, K. Matuud, M. Ashburner, M. Batalo, S. Casavant, T. Plaischman, M., Gasterland, T. Gissi, C., King, B. Kohiwa, H. Kuchi, P. Leeis, S. Wattuu, Y. Mishido, I. Seelo, G. Casavant, T. Radorali, R. Schridl, L. W. Steubli, F. Sutuki, R. Tonata, M. Wagner, L. Washlo, C. Shai, K. W. Makado, I. Seelo, G. Caning, P. & Genniad, R. Matuud, Y. Mishido, I. Sutuki, R. Tonata, M. Wagner, L. Washlo, R. Shai, K. W. Modo, T. Puruno, M. Aono, H. Baldarali, R. Barsh, G. Blake, J. Befelli, D. Bojunga, M. Carindo, M. F. Brownsen, M. J. Bull, J. Mishido, M. Walto, M. Man, M. M. Man, M. Man, M. Man, M. Man, M. Ma	winches—Conferies A Yoohida, K., Hadesgawa, Y., Kawaji, H., Kohtenki, S. and Hayashizaki, Y. Kamaji, H., Kohtenki, S. and Hayashizaki, Y. 685-690 (2001) B. 1006560 B. 21006560 B. 2117651 S. S. Harm. Analysis of he mouse transciptome based on functional annotation of 60,770 (Mull-length CONAC) C. Golge, C. Carlincie, P. Windle, T., Aono, H., Arai, A., Arakwa, T., Eboo, H., Carnincie, P., Pukuda, S., Phumishi, Y., Arakwa, T., Eboo, H., Carnincie, P., Pukuda, S., Phumishi, Y., Arakwa, T., Eboo, H., Carnincie, P., Pukuda, S., Phumishi, Y., Hareoka, T., Boo, H., Carnincie, T., Mani, Y., Hareoka, T., Rothi, L., Toorai, K., Mali, Y., Hareoka, T., Rothi, L., Toorai, K., Too, H., Carnincie, T., Mani, Y., Mali, Y., Too, H., K., Cani, M., Mali, M., Mani, M., Kouda, M., Konaca, K., Rain, M., Kolma, M., Kouda, M., Konaca, K., Mani, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Konaca, M., Mani, M.	
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0; Mismatches 89; Indels 0;
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Nigaea, K. Magodea, Sasaki, M. Carninci, P. McChono, H. Akiyana, J. Nishi, K. Kiteunai, F. Trahito, H. Ichi, M. McKamura, S. Hazama, M. Nishine, M. Tahiti, V. McKamura, S. Hazama, M. Nishine, M. Hateunceo, R. Sakaguchi, S. T. Kegani, T. Keshivagi, K. Pujiakae, S. Inone, K. Togawa, Y. Izawa, M. Ohara, K. Mathiki, M. Yonda, Y. Lankae, T. Marama, M. Ohara, R. Machiki, M. Wonda, Y. Lankae, T. Maramka, T. Mateuura, S. Kawai, J. Marka, I. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. Maramka, M. 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Manure 420, 563-573 [2002]

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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mus musuculu 12 days embryo spinal ocar CDBA, RIKER KULI-length
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CHANNEL BETA-3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT) homolog
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Nature 409 (6821), 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rattus norvegicus), full insert sequence.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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Mus margolis ES celle CDNA, NIKEW full-length enriched library,
SEGRET, GROUPS CHARMEL BETA, SUBUNIT) homolog [Rattus
moryagicus], full linert sequence.
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Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                 556 GGRATGGCAGGAGGACCTGCAGGACGTGTCCATGACTGTGCTCAAGGTCACTGTGAACG 715
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High-efficiency full-length cDNA cloning
Meth, Bnzymol. 303, 19-44 (1999)
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|dev_erage="12 days embryo"
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Katch, H., Kawai, J., Kojian, Y., Komo, S., Komo, H., Woud, M.,
Nakamura, M., Wishil, K., Nomus, K., Numashi, H., Murata, M.,
Nakamura, M., Wishil, K., Nomus, K., Numashi, R., Chin, M., Ohsto, N.,
Sanch, H., Sankai, D., Shibata, K., Mintagawa, R., Shitaki, K., Sakamuma, M.,
Sankai, D., Shibata, K., Shitagawa, A., Shitaki, T.,
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Sepondic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
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VANNEL BETA 3 SUBUNIT (SODIUM CHANNEL BETA 3 SUBUNIT)
homolog [Rattus norvegicus] (SPTR[Q3JK00, evidence: PASTY,
99.5%10, 100%length, match=646)
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Please visit our web site for further details.
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Manysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNNs
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Fax:81-45-503-9216)
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M. Konno, H., Okazaki, Y., Muramarea, H. and Bayabhashi, Y.
Mormalization and subtraction of cop-trapper-edered compass to perspect chil. Length color. Illustrates in En. 1990 edeter of Cop-trapper-edered Compass to perspect chil. Length color. Illustrates in En. 1990 discovery of new wengl. K. Philakes, S. Inoue, X. Izawah, W. Ohara, S. Marchiki, M. Yoneda, Y., Tahikan, T. Tonaka, T. Tanaka, T. Tanaka, T. Tanaka, T. Tanaka, T. Hanka, R. Hayashizaki, Y. Woneda, Y., Kara, A. Muramalisu, M. Inoue, Y., Kira, A. and
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781: 81-45-503-922
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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dev stage="0 day neonate"
lab_host="DH10B"
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UI-M-BH3-bsq-d-04-0-UI.rl WIH BMAP M 54 Mus musculus CDNA clone
UI-M-BH3-bsq-d-04-0-UI 5', mXNA sequence.
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                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                      DB 10; Length 672;
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41.6%; Score 524.4; DB 10; Length
Best Local Similarity 87.0%; Pred. No. 1.18-121;
Matches 576; Conservative 0; Mismatches 66; Indels
Matches 576; Conservative 0; Mismatches 66; Indels
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242 ATGGCCACCAGGAGGTGGAGAGCCCCTTCCAAGGTCGTCTGCAGTGGAATGGGAGCAAAG 301
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Ggi-bin/cluster.cgi/meeq-cSODPF005BB01QF1scluster=6147.r. Contact
Feng Lidang Man.l. f.kinagakifsteech.com WRL.; Falkillengshi, Navitzogen.com/ RNL; Falkillengshi, Navitzogen.com/ INVA; TOGDF005BB01QF1.
Faraday Avenue denoscope acquence ID : CSODF005BB01QF1.
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On Feb 13, 2001 this sequence version replaced gi:12797629.
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AL534136 Homo sapiens PETRI BRAIN Homo sapiens CDNA Clone
CSODPO05Y103 S-PRINE, MRNA sequence.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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CDNA Library preparation: Dr. M. Bento Soares, Universary of Iowa
DNA Sequencing Dr. M. Bento Soares, Universary of Iowa
DNA Sequencing Dr: Dr. M. Bento Soares, Universary of Iowa
Glone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: MJ RWPRSS.
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41.3%; Score 521.4, DB 12, Length 636, Best Local Similarity 88:8%; Preed. No. 5.3-121, Maken 61, Matches 64, Conservative 0, Mismatches 71, Indels 0, Matches 64, Conservative 0, Mismatches 71, Indels 0,
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*Notes="Organic eps" (Vector: PCMV-SOQR76; Oise 1: Not1)

Site 2: Sall; Cloned uniditectionally; Oiso-dr primed.

*Novergie is a sis a NHH MGC Library."

Note: this is a NHH MGC Library."
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Control distribution: WGC Clore distribution information can be found the Liw A. G. Consortium/Luffu at:
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Pred. No. 1.1e-118;
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National Institutes of Health, Mammalian Gene Collection (MGC)
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331 c 402 g 214 t 33 of
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
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Best Local Similarity 91.5%;
Matches 589; Conservative 5
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536 TGGAGGCCACCACCACGTGGTGGTATGGTTCTACAGGCCCGAGGGCGGGTAAAGATTTCCTTA
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                             CA749311
UT-H-F10-cdd-k-17-0-UI.:I NHE MARP_F10 Mus musculus CDNA clone
IMAGE: 6811594 5', mRNA sequence.
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AUTHORS
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825 bp mRNA linear EST 17-JUL-2002 UL-4-200-418-0-UL: 1 NIH BAAP EXO Mus musculus CDNA clone TRADES: 790281 5', mRNA sequence.
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                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5769987"
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Location/Qualifiers
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10 (Nases 1 o 169) oric inf. gov. Nat. Hoto. Collection (NGC) Mat. Ord. Chtc.) (Most. Ord. 1 Institutes of Health, Mammalian Gene Collection (NGC)
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Score 447.2; DB 13; Length
Pred, No. 4.3e-102;
0; Mismatches 88; Indels
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Contact: Robert Strausberg, Ph.D.
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Query Match
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Matches 557; Conservative (
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Pred. No. 6e-81;
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1. 742
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                                                                                  /mol_type="mRNA"
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Banali: cgapba-remail.idh.gov
Ilsene Percuerent: Dr. Jah. idh. University of Iowa
Tisene Percuerent: Dr. Jah. idh. University of Iowa
DNN Library Pregnatation: Dr. M. Bento Soares, University of Iowa
DNN Sequencial by: Dr. M. Bento Soares, University of Iowa
NN Sequencial by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information and the property of Iowa
This clone was contributed by the Brain Molecular Anstomy Project
(SWAP)
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GENERAL INFORMATION:
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Ream No. 6232106
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ADDRESSER: JACORSON, PRICE, HOLMAN & STERN, PPLC
STREET He Jennier Building, 400 Seventh Street, N.W.
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                      Sequence 16, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
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LOCATION: (1)...(15233)
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       RESULT 3
US-09-128-155-16/c
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TITLE OF INVENTION: PRAFI, A No. 6013500el Gene Encoding A Serine/
TITLE OF INVENTION: Threonine Kinase
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CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM LLP
STREET: 1185 Avenue of the Americas
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MEDIUM TYPE: Floppy of
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New York
Y: U.S.A.
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US-09-082-737-1
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PRIOR APPLICATION DATA:

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APPLICANT: Resears A Aidoc
APPLICANT: Resears A Aidoc
APPLICANT: APPLICANT: IN A BEQUENCE Encoding Enzymes of Clavulanic
PRESENTE OF INVESTIGN: INA Sequence Encoding Enzymes of Clavulanic
PRESENT OF AIGOCATION: AGIL Biosynthesis
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IMP Companie PC Companie
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                 ATORNEY AGENT. INFORMALLY...
ATORNEY AGENT. INFORMALLY...
NAME: D. Douglas Price
REGISTRATION UNDERR: 24,514
REGISTRATION UNDERR: 24,514
TELEPROPERATION: 1202 538-5666
TELEK: RCA 42659 1D69 UR
TREEK: RCA 42659 1D69 UR
TROUMATION FOR EQUI DNO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1668 base pairs
TENGTH: 1668 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILIKO DATE: 29-2AV-1997
ATTORNEY/AGBNT INFORMATION:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/726,614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09726614
Patent No. 6514735
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
US-09-385-028-20
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Douglas Price
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy of
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APPLICANT: Susan E. Jenean
APPLICANT: Asian E. Jenean
APPLICANT: Asian S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Parent No. 6232106
FORESTORMENTOR: ALGE Biosynthesis
NOMBER OF EXCURRENCES: 25
ADDRESSE: ADGRESSE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1230 cececesarcescardasesesaserserseacuricesercesesear 1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.9%; Score 36.4; DB 4; Length 1668; 47.4%; Pred. No. 3.7; tive 0; Mismatches 121; Indels 0.
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REPRESIDENCY NUMBER: 24.514
REPRESIDENCY NUMBER: 24.5145/57452052
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 68.666
TELEFAL: (20.7) 5910519
TELECT: RCL 246593 IDEN UR
INFORMATION FOR SEQ ID NO: 20.
SEQUENCE CHARACTRESITICS:
LENGTH: 1669 base pales
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REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMONICATION INCENARION:
TELECOMONICATION INCOMATION:
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FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILLING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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Patent No. 6232106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
NOLECULE TYPE: DNA (genomic)
US-09-726-614-20
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U.S.A.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 36.4; DB 3; Length 11604; Sest Local Smilarity 47.4%; Pred. No. 7.4; Matches 109; Conservative 0; Mismatches 121; Indels 0;
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COMPUTER: IRN PC compatible
OPERATING SYSTER, PC-DOSA(WS-DOS
OPFWARE: Petentin Release #1.0, Version #1.30 (EPO)
CURRET APPLICATION DATA:
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APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
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; Sequence 13, Application US/09726614
; Fatent No. 6514735
; GENERAL INFORMATION:
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REGISTRATION UNDERS. 14.114
RESERVATOR DESCRIPTION
TELECOMMUNICATION TOWNS OF TELEFORM (100 439-666
TELEFORM (200 439-666)
TELEFORM (200 439-669)
TELEFORM (200 439-69)
TELEFORM (200 439-69)
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TELEFORM (200 439-69)
TELEFORM (200 439-69)
TELEK: (202) 3905550
TELEK: RCA 248591 IDBA UR
INCORATION FOR SEG ID NO: 13;
SEGUENCE CHARCTERISTICS:
LENGTH: 11604 base pairs
TYPE: nuclaic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-385-028-13
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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8258 ÚCTCGÁCGGCTÁCAAGCACTTCGACCGCTAČCCGGTCGGCCCCGAGGGACCCACGGCGACCT 8317
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                                                                                                                                                                                                                                                       618 CCAGGAGGTGGAGAGCCCCTTTCAGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTGCA 677
                                                                                                                                                                                                                                                                                                                                                678 GGACGIGICCAICACIGIGCICAACGICACICIGAACGACITCIGGCCICIACACGCGGCAA 737
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                                                                                                                                                                                                           0, Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  798 CCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCT 847
                                                                                                                                                           Query Match 2.9%; Score 36.4; DB 4; Length 11604; Best Local Similarity 47,4%; Parcel No.7.4; Indels Natches 121; Indels 0; Matches 109; Conservative 0; Mismatches 121; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSER: JACOSBOM, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CORRENY FPDIACATION DATA: US/09/385,028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
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FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6232106
GENERAL INFORMATION:
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APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
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REGISTRATYON NUMBER: 24,514
REFERENCE DOCKET NUMBER: 141
TELECOMMUNICATION INFORMATION:
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LENGTH: 11604 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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COUNTRY: U.S.A.
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US-09-385-028-1
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linear

TOPOLOGY:

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Ferrara, Napoleone
Fong, Sherman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-996-243-388
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                                                                                                                                                                                            0; Gaps
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DEPLICANT: Name B. Jonean
APRILOANT: Name A. Aidox
APRILOANT: Name A. Aidox
TITLE OF INVENTION: DA Sequence Encoding Enzymes of Clavulanic
Peter No. 651473

TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES. 15
NUMBER OF SEQUENCES. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   798 CCCCTAAGAGTCACGGAGGCTGGAGGACTTCACCTCTGTGGTCT 847
                                                                                                                                          Query Match 2.9%; Score 36.4; DB 3; Length 15079; Best Local Similarity 47.4%; Pred. No. 8.1; Sest Local Similarity 67.4%; Pred. No. 8.1; Indels 0; Matches 109; Conservative 0; Mismatches 121; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: JACOBSON, PRICE, HOLMAN & STERN, PPLC
The Jenifer Buliding, 400 Seventh Street, N.W.
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NAME: Diouglas Price.

NESTRANCE/DOCKET NUMBER: 1418/PS7452US2
TRESCHONDICATION NUMBER: 1418/PS7452US2
TRESCHOOL (2012 508 4666
TRESCHOOL (2012 508 4666
TRESCHOOL (2012 508 4666
TRESCHOOL (2012 508 4666
TRESCHOOL (2012 508 4666
TRESCHOOL (2012 508 4666)
TRESCHOOL (2012 508 4669)
TRESCHOOL (2012 508 4699)
SUDJUNCTURA (2012 508 4699)
SUDJUNCTURA (2012 508 4699)
MOLECULE TYPE: DNA (genomic)
AYPOTHETICAL: NO
AYPOTHETICAL: ORGINAL SOURCE:
ORGANISM: Streptomyces clavuligerus
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PRIOR APPLICATION NOMBER: US 08/790,462
FILING DATE: 29-0An-1997
ATYORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/726,614
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6514735
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nucleic acid
EDNESS: single
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U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-726-614-1
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                                                                                                US-09-385-028-1
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                                                                                                                                                                                                                                                                                                          Ouery Match Sailarity 47.4%; Pred. No. 96.1, 12 Length 15079; Best Local Sailarity 47.4%; Pred. No. 96.1, 12, Indels 0; Matches 109, Conservative 0; Mismatches 121, Indels 0;
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HYPOTHETICAL: NO
SORIGINAL SOURCES:
ORGANISM: Streptomyces clavuligerus
US-09-726-614-1
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Patent No. 6478825
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Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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** APPLICATION NUMBERS 66/090842
*** PAPLICATION NUMBERS 66/090842
*** APPLICATION NUMBERS 66/090857
*** APPLICATION NUMBERS 66/090857
*** APPLICATION NUMBERS 66/090867
*** APPLICATION NUMBERS 66/09087
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*** PRILING NUMBERS 66/09089 PRIOR PILING DATE: 1998-06-26
PRIOR APLICATION NUMBER: 60/091360
PRIOR PILING DATE: 1998-07-01
PRIOR APLILACTION NUMBER: 60/091478
PRIOR PLING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-07
PRIOR PLING DATE: 1998-07-07 R FILING DATE: 1998-06-24

R PLIANG DATE: 1998-06-24

R PLIANG DATE: 1998-06-24

R R APPLICATION NUMBER: 60/090472

R FILING DATE: 1998-06-24

R PLIANG DATE: 1998-06-24 R PILLING MATE: 1,991-66-19
R APPLICATION NUBBR: 66/108952
R PILLING MATE: 1,995-60-19
R PILLING MATE: 1,995-60-19
R PILLING MATE: 1,995-60-20
R PARICATION NUBBR: 66/109052
R PILLING MATE: 1,995-60-22
R PILLING MATE: 1,995-60-22
R APPLICATION NUBBR: 66/109052
R APPLICATION NUBBR: 66/109052 # FILING DATE: 1998-66-22
R APPLICATION WINGER: 60/00349
R FILING DATE: 1998-06-23/00345
R FILING DATE: 1998-06-23
R FILING DATE: 1998-06-28
R FILING DATE: 1998-06-28
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R FILING DATE: 1998-06-29 FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
FILING DATE: 1998-06-24 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 APPLICATION NUMBER: 60/090431 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090444 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-06-25 PRIOR

R FILING DATE: 1,598,-66.05.
R PALLACATOR WASHER 6.05.
R APPLICATION UNDERS: 60,08655.
R APPLICATION UNDERS: 60,08655.
R APPLICATION UNDERS: 60,08655.
R APPLICATION UNDERS: 60,08653.
R APPLICATION UNDERS: 60,08734.
R APPLICATION UNDERS: 60,08734.
R APPLICATION UNDERS: 60,08736. R PILLM NARE: 1398-06-10, OFFER PROPERTY OFFER PROP R APPLICATION NUMBER: 60/088030
R APPLICATION NUMBER: 60.604
R APPLICATION NUMBER: 60/088033
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088028 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 4098-06-16
PRIOR APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 PRIOR FILING DATE: 1998-06-16 PRIOR APPLICATION NUMBER: 60/089514 LICATION NUMBER: 60/088742 FILING DATE: 1998-06-11 FILING DATE: 1998-03-20 FILING DATE: 1998-05-07

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1043 GNGGIGGCCTGARCACCTGAGGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCA 1102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                  APPLICANT: DORNER, F.
APPLICANT: SCHEFFLINGER, F.
APPLICANT: FALKERE, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
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FD: 30472/114 IMMU
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 19, Application US/09320878A
; Patent No. 6117659
                                Sequence 14, Application US/08232463; Patent No. 5670367; GENERAL INFORMATION:
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FELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 26-AUG-1991
ATTORNEY/AGBYT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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          US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1824 CAGGCCTCACAGCACCCAGGCATGGGGACGTGGGCCAGTCTGGGCCCCCCTGGCCTGTTGC 1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 GCGCTTTRAGGACCCGCGTGTCTTCGGATCCTGAGCGGTACGATGCCTCCATCCT 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 GACGCCGACTCTCCGTGCTGAGCCCCGGCGAGCGGGCGCGGGGCGCCTGATCGGCT 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     573 CGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      327 CÓGGGGACCTGAGCAGTÍTGTATTCTACTACCACATAGAÍCCCTTÓCAACCCATGAGTGG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             633 CCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTGCAGGACGTGTCCATCAC 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           693 TGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 CTGGGCGCAAACGAGCGAGGCAGGGCGCGCGAGTGGAAGCTGGAGTTCCGGGGTGGGCGGG 85
                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                       2.9%; Score 36.2; DB 4; Length 1371;
49.2%; Pred. No. 3.9;
tive 0; Mismatches 98; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APAIL OWNT Nessen et al. 1710 00 Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Proteins Prints Parts 2001-07-16 Parts Prints Parts 2001-07-16 Parts Prints Parts 2001-07-16 Parts Prints Parts 2001-07-16 Parts Prints Parts Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prints Prin
PRICE FILING DATE: 1998 0-0°02
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PRICE FILING DATE: 1998 0-0°07
PRICE PRICE PRICE DATE: 60°07
PRICE FILING DATE: 1998 0-0°07
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Patent No. 6566225
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-07-09
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                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 49.2
Matches 95; Conservative
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, OKGANISM: Homo sapiens
US-09-904-615-16
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SEQ ID NO 16
LENGTH: 2608
                                                                                                                                                                                                                                                                                                                                                  Query Match
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153 ACTGGGGAGGTCCAGTGGGGTCGCTTAGGGCCCCAAAGCCCCCACCCGGCTCCAAAAGCTC 212
BEARLER RITHING DAFF, 1997-04-30
ENALIER APPLICATION WHERE: PROV. 60/076,919
BARLER PILING DAFF, 1996-03-05
ENALIER RITHING DAFF, 1996-03-05
ENALIER RITHING DAFF, 1996-03-08
WHERE RO ENGL 19 1996-05-29
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*** APPLICANT: BTRACH, Welanie C.
*** APPLICANT: BTRACH, Welanie C.
*** APPLICANT: BTRACH, Welanie C.
*** APPLICANT: WORDANIE, Robert
*** APPLICANT: WORDANIE, Robert
*** APPLICANT: WORDANIE, Robert
*** TITLE OF INVESTION: Combinatorial PolyMetide Libraries Produced Using a FILE SPERMET. ON ACTIONATION ROBE CONCERNIT APPLICANTON NUMBER: US/99/141,908
*** CURRENT FILITANIE MARF: 199-69-28
*** BARLIER PRILICANIEN BUNES: GTO 0F 09/07):538
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                                                                       APPLICANT: ASHLEY, GAP.
APPLICANT: BIRTAGH, MARY C.
APPLICANT: BIRTAGH, MARY C.
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APPLICANT: HOLDMIEL, Robert
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EARLIER APPLICATION NUMBER: 60/087,080
EARLIER FILING DATE: 1998-05-28
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; Patent No. 6503741
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
                              GENERAL INFORMATION:
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Sequence 13. Application US/09657440

GENERAL INCOMMENTOR

APPLICANT. SETLACH, Melanie C.

APPLICANT. BETLACH, Melanie C.

APPLICANT. BETLACH, May C.

APPLICANT. WCANATEL, Pobert

APPLICANT. WCANATEL, Pobert

APPLICANT. WAS . M.

TITLE OF TUNKNINON. WROEBE. 19/90457,440

CURRENT FLINO DATE. 2006.2200120

CURRENT FLINO DATE. 2006.29-07

FRIOR APPLICATION MURBER: 09/320,878

FRIOR FLINO DATE. 1999-06-27

FRIOR FLINO DATE. 1999-06-27

FRIOR FLINO DATE. 1999-06-37

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Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0 Total number of hits satisfying chosen parameters: 4403344

2201672 segs, 1661799599 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0*

Maximum Match 100% Listing first 45 summaries

| Published_Applications_NA. |
1. (Aggraf, Exponders/l), Dubbra/1897	PubCoMB.seq:
2. (Aggraf, Exponders/l), Dubbra/1897	PubCoMB.seq:
3. (Aggraf, Exponders/l), Dubbra/1896	PubCoMB.seq:
4. (Aggraf, Exponders/l), Dubbra/1896	PubCoMB.seq:
5. (Aggraf, Exponders/l), Dubbra/1896	PubCoMB.seq:
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14. (Aggraf, Exponders/l), Dubbra/1896	PubCoMB.seq:
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16. (Aggraf, Exponders/l), Pubpra/1896	PubCoMB.seq:
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18. (Aggraf, Exponders/l), Pubpra/1896	PubCoMB.s

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and its derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 4, Appli	Sequence 22. Appl	Sequence 1, Appli	Sequence 3, Appli	21,	Seguence 7659, Ap	Sequence 23, Appl			Sequence 2514, Ap	Sequence 1435, Ap	Seguence 58, Appl	Sequence 59, Appl	Sequence 102, App	Seguence 3, Appli	
	D De	US-09-997-579-4	US-10-029-191-22	US-10-029-191-1	US-09-997-579-3	US-10-029-191-21	US-09-764-891-7659	US-10-029-191-23	US-09-917-800A-1654	US-10-029-386-16214	US-10-029-386-2514	US-10-017-161-1435	US-09-771-161A-58	US-09-771-161A-59	US-09-291-417-102	US-10-134-102-3	US-09-960-352-2238
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oko	Query	100.0	44.4	44.4	42.8	42.4	17.1	11.8	11.0	9.	9.0	3.3	3.3	3.3	3.5	3.5	3.2
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Sequence 20, Appl	-	Sequence 20, Appl	Sequence 20, Appl		20,	50,	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl		Sequence 20, Appl	63,	Sequence 120, App			Sequence 24925, A	Sequence 7698, Ap	Sequence 142, App	185	Sequence 9, Appli	17,	Sequence 87, Appl	Sequence 55, Appl	14,	3077		Sequence 215913,
US-10-140-472-20	US-10-141-761-20	US-10-142-885-20	US-10-158-790-20	US-10-137-871-20	US-10-140-805-20	US-10-140-864-20	US-10-140-923-20	US-10-141-756-20	US-10-141-759-20	US-10-123-155-20	US-10-146-731-20	US-10-094-466-63	US-10-120-988-120	US-10-029-386-22980	US-09-974-300-836	US-10-029-386-24925	US-09-815-242-7698	US-10-120-988-142	US-10-017-161-1857	US-10-102-622-9	US-10-102-622-11	US-09-893-519A-87	US-10-034-650-55	US-09-999-121-14	US-10-027-632-30772	US-10-027-632-30772	US-10-027-632-215913
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39.2	39.5	39.2	39.5	39.2	39.5	39.2	39.2	39.5	39.5	39.2	39.2	39.2	39.2	39	39	38.6	38.6	38.6	38.4	38	38	38	38	38	37.8	37.8	37.8
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ALIGNMENTS

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ψp	Query Match Best Local Similarity	100.0%;	Scor	Score 1261; Pred. No. 0;	DB	10,	Score 1261; DB 10; Length 1261; Pred. No. 0;	1261;				
2	Matches 1261; Conservative		Ţ,	0; Mismatches			0; Indels	0,	0; Gaps	0,		
à	1 CCTCCCTTCCGAGCTGAGCTTACCCTGGGCGCAAACGAGCGAG	GAGCTGAGC	TTACC	TGGGCGC	AAAO	3AGC	SAGGCAGG	99090	AGTGG	09		
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Best Local Smilarity 84.44; Pred. No. 3.8e-160;
Matches 655; Conservative 0; Mismatches 114; Indels
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[120] GACTOCCTAAACTCGATCAGACTCTAGGACACATAAAGACGCG 1260
[120] GACTOCCTAACTGACACACATAAGACACTTAGGACGC 1260
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181 GGCCCAAAGCCCCAGCCGGCTCCAAAAGCTCCGAGGGCCTCCCAGGGACCGGGGGCCCGAGGGCCCAGGGCCCAGGGCCCCAGGGTCCAAAAGCTCCGAGGGCCTCCCAGGGCCCCAGGGTCCTCG 240
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241 GCCCTTCCTTCGGTCAGAAGTCGCCCCTGGGGGCAATTCGTCCCAAAGGGTTTCCTCG 300
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730 432 790 971 TTGCCATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAATAGAACAGGA 1030

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971 TIGCCATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAATAGAACAGGA 1030
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                                       911 ATTGCTACAGAAGGTCTCAAAAGCCGAAGAGCGCCCAAGAAAACGCGTCTGACTACC 970
                                                                                  613 ATTGCTACAGAAAGGTCTCTAAGGCCGAAGAGGCACAGGAAAATGCGTCTGACTACC 672
                                                                                                                                                553 AAATCATGATGTACATCCTCCTGGTCTTCCTCACCTTGTGGCTGTTTATTGAGATGATCT 612
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42.8%; Score 540; DB 10; Length 2220;
Best Local Similarity 69.3%; Pred. No. 3.4e-120

Matches 582; Conservative 0; Mismatches 70; Indels 0; Gaps
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US-09-997-579-3
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Secures 1, Application US/10029191
SENBIRAL INFORMATION:
GENERAL INFORMATION:
APPLICAN: GORTA, SORY A.J.
ATTLE OF INFORMATION:
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CHERER SENBIRAL TO 47 0 0002/10
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ATTLE OF INFORMATION: NOTE: 0.001-0.21
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ATTLE OF INFORMATION: 0.001-0.001
BELIOR PRILING DATE: 2000-0.001
BELIOR PRILING DATE: 1.000-0.001
BELIOR PRILING DATE: 1.990-0.14
NUMBER OF SEQ. ID NOS: 2.1
SEQ. ID NOS: 2.1
                                                              1031 GCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCAGCAATG 1090
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727 Gresierektrigagerearcre-aerecteaeacresararceceartreaere 785
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                                                                                                                                                193 ATCCCATGAAGCTGAAGTGCATCTCCTGCATGAAGAGGGGAGGAGGAGGAGGCCACTG
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                                                                                                                                                                                    Match 1-10cal Similarity 44.4%; Score 559.6; DB 13; Length 3108; Local Similarity 94.4%; Pred. No. 46-160; Conservative 0; Mismatches 114; Indels 7; tas 55; Conservative 0; Mismatches 114; Indels 7;
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US-10-029-191-1
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                     796 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC 855
                                                                     421 ATACCTTTGCGAGTCACTGAAGAGCGGGGAGAAGACTTCACCTCCGTGGTCTCGGAAATC 480
                                                                                                                                                                                                                                           916 TACAGAAAGGTCTCAAAAGCCGAAGAGCAGCCCAAGAAAACGCGTCTGACTACCTTGCC 975
                                                                                                                                                                                                                                                                          33 AGGIGGCCTGAACACCTGAGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCAG 92
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TITLE OF INVENTIOR: PROFILE BENCALING A SODIUM CHANNEL BEPA-3 SUBUNIT TITLE OF INVENTIOR: PROFILE BENCALING A SODIUM CHANNEL BEPA-3 SUBUNIT TITLE OF INVENTIOR: PROFILE BINCORY, SOUTH OF THE BEREBRICH S. 210.14.7. 00XX/591.
CURRANT APPLICATION NUMBER: US/50.9.9.
PRIOR APPLICATION NUMBER: US 60/134, 198
PRIOR ELING DATE: 3000-05-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 CAFCCATACATCCACCTGTGTGACTTTCACCTGTGACTCCTAACTCCATCAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.1%; Score 216; DB 11; Length 4625; 100.0%; Pred. No. 4.2e-55; tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHICLORY: Resen et al. TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies UTITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies CHRENT APPLICATION UNDERS: US/09/764,891
CHRENT FILEN DATE: 200.00-11/9
Prior application data removed - consult PALM or file wrapper SOFWARE: Patent Nucl. 2.0
                                                                                                                                                                                                                                                                                                                                                    976 ATCCCATCTGAGAACAAGGGAACTCTGCGGTACCAGTGGAGGAA 1020
                                                                                                                                                                                                                                                                                                                                                                                               601 ATCCTTCAGAGACAAGGAGAACTCTGTGGTACCTGTGGAGGAA 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7659, Application US/09764891, Publication No. US20030077808A1, GENERAL INFORMATION:
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Publication No. US20020160453A1
GENERAL INFORMATION:
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Matches 216; Conservative
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US-09-764-891-7659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AATGPGTCCAGGAGTTCGAGGCACACAGGCCTTTTGTGAGACCACAGAGACTG 420
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                                                                                                                                                             851 AAATCATGATGTACGTTCTTCTTCTTCTCACCCTGTGGCTGCTCATCGAGATGATAT 910
                                                                                                                                                                                               838 AAATCATGATGTACATCCTCCTGGTCTTCCTCACCTTGTGGTTTATTGAGATGT 897
                                                                                                                                                                                                                                                                                                        791 GGCTGATCCCCCTAAGAGTCACCGAAGAAGCTGGAGAGGACTTCACCTCTGTGTGTCTCAG 850
                                                                                                    778 GACTIGATACCTTTGCGAGTCACTGAAGAGGGGGGAGAAGACTTCACCTCCGTGGTCTCGG 837
                                                                                                                                                                                                                                                                          911 ATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAAGGCGTCTGACTACC 970
718 CATGCAATGTGTCCAGGGAGTTCGAATTCGAGGCACACAGGCCTTTTGTGAAGACCACGA 777
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PRICE REPERINGE: 2001-12-20

PRICE FILLY DATE: 2001-12-20

PRICE FILLY DATE: 3000-05-12

PRICE FILLY DATE: 3999-05-14

PRICE FILLY DATE: 3999-05-14

PRICE FILLY DATE: 3999-05-14

PRICE FILLY DATE: 3999-05-14
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Publication No. US20020160453A1
GENERAL INFORMATION:
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US-10-029-191-21
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Best Local Similarity
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; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_017288
US-09-917-800A-1654
    ORGANISM: Rattus norvegicus
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Pred. No. 1e-34;
0; Mismatches 223; Indels
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APPLICANT Obneson, Kory
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GURRANT APPLICATION NUMBER: US 60/222,040
PRICE FILING DATE: 2000-07-31
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 657
                                                                                                                                                                                                      Query Match
Best Local Similarity 57.71
Matches 333; Conservative
                                                                                                       ; TYPE: DNA
; ORGANISM: Lepus Sp.
US-10-029-191-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                             622 GAGGTGGAGAGCCCCTTTCAGGGCGCCTGCAGTGGAATGGCAG-----CAAGGAC 672
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Ouery Match 11.0%; Score 138.6; DB 10; Length 1490; Best Local Similarity 5.7%; Pered. No. 1.22-23; Best Macches 237; Conservative 0; Mismatches 239; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               970 CTTGCCATCCCATCTGAGAACAAGAAGACTCTGCGG 1006
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Sequence 16214, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:

US-10-029-386-16214

RESULT 9

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62 TATGAGAATGAGGTGTTGCAGCTGGAGGAGGATGAGCGCTTCGAGGGCCGCGTGTGGTGTGG
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                                                                                                                                                              CTHEN THRORMATION: MISSENCH THI: 0,00549, EVALUE 6.006-42
OTHEN THRORMATION: NT HIT: U12191.1, EVALUE 0.006-10
U5-10-123-366-2514

TO THEN THRORMATION: EST_HUMAN HIT: B1754689.1, EVALUE 0.006-10
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 569;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
3.9%; Score 49; DB 12;
Best Local Similarity 60.1%; Pred. No. 0.00019;
Macches 104; Conservative 0; Mismatches 60;
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LOCATION: (133)..(T34)
OTHER INFORMATION: a, t, c, g, unknown or other
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Publication No. US20030143668A1
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OTHER INFORMATION: a, t, c, g,
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LOCATION: (124)..(125)
OTHER INFORMATION: a, t, c,
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OTHER INFORMATION: a, t, c,
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LOCATION: (127)..(128)
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(1)..(922)
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APPLICANT: "Enk, SHARTEN G.

APPLICANT: "Enk, David R.

TITLE OF INVENTION: EXPRESSION ANALYSIS TWO.
FILE DEFENDENCE: HOMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C.
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OTHER INFORMATION: EXPERSESED IN ILPNG SIGNAL = 1.3

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OTHER INFORMATION: EXPERSESED IN HEATH, SIGNAL = 1.2

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OTHER INFORMATION: EST-HUMAN HIT: BF953777.1, EVALUE 1.006-129
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OTHER INFORMATION EXPRESSED IN 1976, STGNAL = 1.2
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OTHER INFORMATION EXPRESSED IN BEALA, STGNAL = 3.7
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ORGANISM: Homo sapiens
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; NAME/KEY: modified base; LOCATION: (415)(417); OTHER HYGORMATION: a, t, c, g, unknown or other; PENTURE:	; NAME/KEY: modified_base; LOCATION: (422); COTHER (422); COTHER (422); FEATURE: (422); FEATURE:	; NAME/KEY: modified base; LOCATION: (439); COTATION: (439); OTHER INFORMATION: a, t, c, g, unknown or other; FRATURE;	; NAME/KEY: modified_base; LOCATION: (441); OTHER INFORMATION: a, t, c, g, unknown or other; FEATURE:	// NAME/KEYTON: modified_base // LOCATION: (443) // OTHER HEYORMATION: a, t, c, g, unknown or other // PRATURE:	NAME/KEY: modified_base; LOCATION: (445) OTHER INFORMATION: a, t, c, g, unknown or other PRATURE:) MANEKKER, modified_base;) LOCATION: (465)); OTHER INFORMATION: a, t, c, g, unknown or other ? FRATURE:): NAME/KEY: modified base): LOCATION: (469)(471)): OTHER INFORMATION: a, t, c, g, unknown or other FRATURE:) NAME/KET; modified hase; LOCATION: (70): (768); O'THER INFORMATION: a, t, c, g, unknown or other PRAKIER.	NAME/KGY: modified base; 1.OCATION: (490)(491) 7. OTHER INFORMATION: a, t, c, g, unknown or other; FRATHER	NAME/KEY: modified_base) MANE/KEY: modified hase) LOCATION: (497). (798)) OTHER INFORMATION: a, t, c, g, unknown or other FRAURE:	NAME/KEY: modified base) MNB/KNY: modified_base) LOCATION: (519)) OTHER INFORMATION: a, t, c, g, unknown or other) FRAUDE:	; NAME/KEY: modified base ; LOCATION: (529)(530) ; OTHEN THORMATION: a, t, c, g, unknown oz other ; FEATURE:	j NAME/KEVE, modified_base j LOCATION: (540) j THER INFORMATION: a, t, c, g, unknown or other FEATURE:	NMME/KET modified base 1.COCATION: [548]. (548) 7. THER INFORMATION: 8, t, c, g, unknown or other prayer.) NAME/KEY: nedified base) COCHION: (564). (564). OTHER IMPORMATION: (a, c, c, g, unknown or other FEATURE: NAME/KEY: modified_base
FEATURE INSERTION OF A UNKNOWN OF OTHER TREORDATION: a, t, c, g, unknown or other OTHER INFORMATION: a, t, c, g, unknown or other	FRAUDEN NAWE/KEY: modified_base 10ARTON: (142). THE TREORMATION: (a, c, c, c, c, c) THEN TREORMATION: (a, c, c, c, c)	PRATURE: modified_base NAME/REF: modified_base LOCATION: (147) OTHER INFORMATION: a, t, c, g, unknown or other	FEATURE IN AMERICAL modified base LOATER INTERIOR (ISI) OTHER INFORMATION: a, t, c, g, unknown or other	PRATURE NAWE/KEY: modified base LOOATRON (311) OTHER INFORMATION: a, t, c, g, unknown or other	: modified_base : (322) FORMATION: a, t, c,	FeATURE: modified_base LOCATION: (326) OTHER IMPORATION: a, t, c, g, unknown or other	FeATURE: modified base NAMB/RET: modified base LOCATION: (345): (345): (340) OTHER INFORMATION: a, t, c, g, unknown or other	PEATURE MANE/KET: modified base LOATION (1817). (1817)	FRATURE NAME/KEY: modified base LOCATION: (364) OTHER INFORMATION: a, t, c, g, unknown or other	PRATURE: modified base NAME/KEY: modified base TOCHTRON: [366][366] OTHER IMPROMATION: a, t, c, g, unknown or other	FeATURE: modified base NAMP/KET: modified base JOCATION: (370): (380) OTHER IMPROMATION: a, t, c, g, unknown or other	FRATURE: modified base LOCATION: (384) OTHER INFORMATION: a, t, c, g, unknown or other	MARIORE: modified base NOGATORE: (380). (380) THERE IMPRODATES A, C, C, G, unknown or other	Namidra modified base Nama Kar (192) The modified base The modified to the mo	NAMENTER: modified base books (394). (359). (359). (750).	FAATURAT. NAMB/KRY: modified base LOCATION: (403) CTER INFORMATION: a, c, c, g, unknown or other	FRATURE: modified hase NAMENTY ST: modified hase DOCHTON: (411) FRATURE: PORMATION: a, t, c, g, unknown or other

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SEQ ID NO 59 LENGTH: 3382

TYPE: DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 GCCGGGCCGGAGTTGCCTCCCGGGGCCCGCGAGGCCCCGCGGGGCGCGCT 199
                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                              3.3%; Score 41.2; DB 12; Length 922;
40.9%; Pred. No. 0.056;
tive 0; Mismatches 101; Indels 0.
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52.0%; Pred. No. 0.069;
tive 0; Mismatches 85; Indels (
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OTHER INFORMATION: a, t, c, g, unknown or other
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                                                                         3.3%
Best Local Similarity 40.9%
Matches 70; Conservative
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                                     NAME/KEY; modified_base
LOCATION: (573)
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Best Local Similarity
Matches 92; Conserv
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LENGTH: 1097
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                           FEATURE:
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Sequence 59, Application U8/09771161A
PRIERE IN. U82002010811A1
GEREAL, INFORMATION et al.
ATTICL OF INVENTION 'VALIANTE OF PROTEIN KINNEES
TITLE OF INVENTION' 'VALIANTE OF PROTEIN KINNEES
CURRENT APPLICATION NUMBER: 185/09/771, 161A

US-09-771-161A-59

RESULT 13

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tive 0; Mismatches 103; Indels 0; Gaps
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December 5, 2003, 14:16:11; Search time 2705.05 Seconds (without alignments) 979:959 Million call updates/sec OM nucleic - nucleic search, using sw model Run on:

648 1 atgootgoottoaatagatt......cggtaocagtggaggaatag 648 US-09-936-680-4_COPY_376_1023 Title: Perfect score: Sequence:

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5777422 Total number of hits satisfying chosen parameters: 2888711 segs, 20454813386 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Gox,P., Dixon,A., Jackson,A. and Morgan,K. A novel family of bete sub-unit proteins from a voltage-gated sodi um channel, nucleic acids encoding them and therapeutic or

REFERENCE AUTHORS TITLE

Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

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                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (28-JUN-1999) Morgan K., Biochemistry, University of
Cambridge, Tennis Court Road, Cambridge, CB2 1QW, UNITED KINGDOM
Revised by [4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-WAR-2000) Morgan K., Biochemistry, University of Cambridge, Temire Cout Road, Cambridge, CE2 10M, UNITED KINGDOM ON Mar 14, 2000 this sequence version replaced gl:7160974.
Location/Qualifiers
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                           Morgan, K., Stevens, E.B., Shaw, B., Cox, P., Dixon, A.K., Lee, K., Falmock, R.D., Highes, J., Richardson, P.J., Mizuguchi, K. and Jackson, A.P.
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Loto, Y., Hirai, M., Terao, K., Suzuki, Y., Sugamo, S. and Hashimoto, K. 
Assignment of 118 novel cDRAs of cynomologus monkey bzain to human
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Macaca fascicularis brain cDNA clone:QmoA-13657, full insert
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                                                                                                                                                                                       Submitted (id-cort-1999) togam others, Assure DNA Research Institute, Listbratted (id-cort-1999) togam others, Assure DNA Research Institute, 229-2081. John (W-manl:cdmainfc@kausa.or.jp, 1827-2913). Fax:http://www.kausa.or.jp/hnge/, Tel:+81-438-52-3913, Fax:+81-488-52-3913.
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/codon_start=_1
/product="XIAN1188 protein"
/protein_id="BA86472.1"
/db_xref="G1:6330136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue type="brain"
clone lib="pBluescriptII SK plus"
dev_stage="adult"
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/mol type="mRNA"
/db_xrefa"taxon:9606"
/clone="hj00081"
                                             2 (bases 1 to 5306)
Obara,O., Nagase,T. and Kikuno,R.
Direct Submission
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// prodei_e="prefit and peart sodium channel beta 3 subunit"
// prodei_e="axiliary protein"
// prodei_e="axiliary protein"
// canslation="WRARRILPLASLULYWYRYCEPVCTEVPSETPANCONSMYCKET
// translation="WRARRILPLASLULYWYRYCEPVCTEVPSETPANCONSMYCKET
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                        RNO243395 29-JAM-2003
Rattus norvegicus mRNA for voltage-gated sodium channel beta-3
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Location/Qualifiers
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Pred. No. 5e-116;
0; Mismatches 69; Indels 0;
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A721395-2 GI:7242802
Sentho Bene; voltage-gated sodium channel beta-3 subunit.
Rattus norvegicus (Norway xat)
Rattus norvegicus
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/mol_type="mRNA"
/mol_type="mRNA"
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/iissue_type="brain"
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A novel family of beta sub-unit proteins from a voltage-gated sodi
un channel, nucleid, acids encoding them and therapeutic or
diagnostic uses there of
Patent: WO 0005137A b 2 6-CT-2000;
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/mol_type="genomic DNA"
/db_xref="taxon:10118"
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               Bukaryotä; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
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Pred. No. 4.9e-116;
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/mol_type="genomic DNA"
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Sequence 21 from Patent 1
AX048004
AX048004.1 GI:11876882
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 82.8%;
Best Local Similarity 89.3%;
Matches 578; Conservative (
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sv_stage="adult"
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/gene="SCN3B"
                                                                                                                                                                                                                                                                                                                                                                                                             tch 82.8%;
al Similarity 89.3%;
578; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGGAGGTGGAGGCCCACCACGGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 CACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGGAACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGCGTG
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Key
Location/Qualifiers
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Pred. No. 5.8e-89;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .471
/organism="Zea mays"
/mol_type="genomic DNA"
/db xref="taxon:4577"
a _126 c 143 g 106
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   Zea mays
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Best Local Si
Matches 433;
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                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                     COMMENT
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                    Lepus sp.
Makaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Lagomorpha, Lepozidae, Lepus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCTGGTTATCTACTGGGTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                     Length 645;
                                                                                                 Curtis,R.A.
Gere encoding a sodium channel beta-3 subunit protein
Parent: NO 1069912-A. 21 23-NOV-2007
Willennium Pharacouticals, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 ATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAA 645
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                                                                                                                                                                                                                                                                                                                                                               Score 534.6; DB 6;
Pred. No. 1.6e-115;
0; Mismatches 69;
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Secreted expressed sequence tags
BD059018.1 G1:22604624
JP 2001519666-A/873.
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 89.3%;
Matches 576; Conservative
                                                                                                                                                                                                                    1, .645
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ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                    ORGANISM
                                                                                                                            TITLE
JOURNAL
                                                                                    REFERENCE
AUTHORS
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120 147 180 207 240 267 300 327 360 420 387 447

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VERSION KEYWORDS SOURCE

TITLE JOURNAL REFERENCE REFERENCE AUTHORS

AUTHORS

TITLE

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17530 CTCTGAACGACTCTGCCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGC 17471
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In (bases 1 to 172546) in Santheria (Santh, D.A.
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15.4%; Score 229.6; DB 2; Length 127347;
Best Local Similarity 96.3%; Pred. No. 1.18-43;
Matches 255; Conservative 0; Mismatches 9; Indels 0;
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       121143: gap of 100 bp
125917: contig of 4774 bp in length
126017: gap of 100 bp
127347: contig of 1330 bp in length.
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HTG; HTGS PHASE1; HTGS_DRAFT; HTGS_CANCELLED.
Homo sapiens (human)
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126018. .127347
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27508 c 27825 g 34989 t
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/clone="7m99-32A1"
1. 3353
/note="assembly_fragment"
33633. 59223
/note="assembly_fragment"
                                                                                                                                                                                                                                                                1. ,127347
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1.15-1 Kitasato Segamihara, Kanagawa 228-6555, Japan (GaC);
(E.mail.hattorièger. criken, go.jp.) Wü.http://hgp.gec.riken.go.jp/,
(E.m. 12.42-778-9524) Raxial-42-778-9524)
On Aug 18, 42-778-9524) Raxial-42-778-9524,
On Aug 18, 2000 this sequence version replaced gi:8118870.
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Web site: http://hgp.gsc.riken.go.jp/
Contact: hattoridgsc.riken.go.jp
Contact: hattoridgsc.riken.go.jp
Contact: project Information
Center project name: HumDraffil
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9 172546: contig of 37128 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 35.4%; Score 229.6; DB 2;
Best Local Similarity 96.3%; Pred. No. 1.1e-43;
Marches 235; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                /clone="RP11-331G19"
/clone lib="RPCI-11"
47530 a 37712 c 38612 g 46556 t
                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/chromosome="Chromosome 10"
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Job time : 2707.8 secs

    172546
    /organism="Homo sapiens"

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                           Smith Dr. 19 (1998) Section 100 Beaver Street States and 100 Beaver Street States and 100 Meaver Street States and 100 Meaver Street States and 100 Meaver Street Waltham, NA 02153, USA CO. Jun 9, 2000 this sequence version replaced gi:7549605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 170446; sum-of-contigs
Quality coverage: 4.3x in Q20 bases; sum-of-contigs
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Sequencing vector. With the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second control of the second 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                Center code: GTC
Web site: http://www.genomecorp.com/
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2189 sape of unknown length length
2189 contig of 1350 bp in length
4562 contig of Mixhown length
6344 contig of Mixhown length
6344 contig of 1682 bp in length
9211 contig of 1777 bp in length
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of 18875 bp in length
unknown length
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of 16343 bp in length
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contig of 6371 bp in length
gap of unknown length
contig of 5012 bp in length
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contig of 2676 bp in length
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of 2770 h
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     (bases 1 to 172546)
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Listing first 45 summaries
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AAF84146
ABA93727
AAK52345
AAH98320
AAC67836
AAC90602
                                                                                                                                                                      - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Morgan

Dixon A, Jackson A,

Query Match 1

Score 648

No. Result

100.0 99.8 99.8 90.3 82.8 82.8

646.4 646.4 585 570.2 536.6 536.6

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The invention provides a novel betal-like sub-unit for voltage-gated codium ion channel polygeptide, predictionly a sensory neurone specific channel (SMS) subunit. The novel betal-like subunit is useful for producting a therapeutic esent which is useful retarting pain in a patient. The subunit can be expressed by standard recombinant methodology. The presents a human novel sodium channel betal-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACCAGAGGTGGAGAGCCCTTTCAGGGGCGCCTGCAGGAATGGCAGCAAGGACCTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel sub-unit for voltage-gated sodium channel proteins for producing agents useful for treating pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 AIGCCIGCCTICAAIAGAIIGITTTTCCCCIGGCTICTCTCGIGCTIATCTACTGGGGTCAGT
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                                                                                                                                                                                                                                                                Sodium channel; sensory neurone specific channel; betal-like subunit; SNS; therapeutic; pain; analgesic; ss.
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Pred, No. 7e-167;
0; Mismatches 1; Indels 0;
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/product= "sodium channel betal-like subunit"
                                                                                                                                                                                                                 Human novel sodium channel betal-like subunit encoding cDNA
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                                                                            Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain, epilepsy and stroke.
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ilarity 100.0%; Pred. No. 2.4e-167;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         Claim 10; Page 70-71; 88pp; English.
    2000-665241/64
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                                                                                                                                                                                                                                                    61 GTCTGCTTCCCTGTGTGTGTGGAAGTGCCCTCGGAGACGGAGACGTGCAGGCAACCCC
                                                                                                                                                                                                                                                                                                                                                                    964 GICTGCTTCCCTGTGTGTGTGTGAAGTGCCCTCGGAGACGGAGGCCGTGCAGGGCAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAAGAGGAGGTGGAGCCACCACGGTGGTG
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                                                                                                                                            Indels
                       Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 other;
                                                             Score 646.4; DB 24;
Pred. No. 1e-166;
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                                                                               99.8%;
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                                                                                                                     Best Local Similarity 99.8
Matches 647; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human CDNA sequences and clones derived from human fetal brain, fetal schiey, melanoma, testis and amygdala CDNA libraries, useful in genetic screening and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            693 ATGATGTACATCCTTCTGGTCTTCCTCACCTTGTGGCTGCTCATCGAGATGATATTTGC
CACCAGGAGGTGGAGAGCCCCTTTTCAGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTG
                                                             CAGGACGTGTCCATCACTGTGAACGTCACTGAACGACGACTGTGGCCTCTACACCTGC
                                                                                                  CAGGACGTGTCCATCACTGTCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC
                                                                                                                                                                                  AATGTGTCCCGGGAGTTTCAGTTTGAGGCGCATCGGCCCTTTGTGTGAAGACGCCGCCTG
                                                                                                                                                                                                                                      AATGTGTCCCCGGGAGTTTGAGTTTGAGCGCCCATCGGCCCTTTGTGAAGACGACGCGGCTG
                                                                                                                                                                                                                                                                                                   ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGGACTTCACCTCTGTGGTCTCAGAAATC
                                                                                                                                                                                                                                                                                                                                                  633 ATCCCCTAAGAGTCACCGAGGAGGCTGGAGACTTCACCTCTGTGGTCTCAGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAATAG 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human signal transduction cDNA clone amy2_2f18.
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                                                      722 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGACTTCACCTCTGTGGTCTCAGAAATC
                                                                                                                              ATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAGATGATATATTGC
                                                                                                                                                           1 ATGCCTGCCTTCAATAGATTGTTTCCCCCTGGCTTCTCTCGTGCTTATCTACTGGGTCAGT
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Pred. No. 4.4e-146;
0; Mismatches 33; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Numan; sheep; pig; cow; fruit fly; yeast; hamster; macaque; htt. comtor; monkey; dog; sea turchin; expressed sequence tag; EST; diagnostics; foremsic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human EST-derived coding sequence SEQ ID NO: 177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ou P, Qian XB, Wang Z,
Zhang J, Werhman T;
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94.6%;
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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Best Local Similarity 94.6:
Matches 612; Conservative
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Cao Y, Drmanac RA,
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P-PSDB; AAM23661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polymucleotides (AAK51455-AAK51435) and the encoded polypedies (AAK51345-AAK51435) and the encoded polypedies (AAK9233-AAK900001 hat exhibt activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of orber cytokines in other cell polymulations. We consider the polymulations was peptide thereapy, vaccines or polymulations was considered to the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideration of the consideratio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAK6020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                Cao Y,
                                                                                                                                                                                                                                                                                                                                            Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y,
Wang D, Wang Y, Zhang J, Ren F, Chen R, Wang ZW;
Yang Y, Wejhrman T, Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1045 BP; 222 A; 289 C; 314 G; 220 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2934-2935; 6221pp; English.
                                                                           2000US-0560B75.
2000US-052025.
2000US-052325.
2000US-0654936.
2000US-065351.
2000US-0728422.
                                                      2000US-0496914
05-FEB-2001; 2001WO-US04098
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                                                                                       01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
                                                                                                                                                                                                                                           30-NOV-2000;
                                                      03-FEB-2000;
                                                                               27-APR-2000;
20-JUN-2000;
                                                                                                                              19-JUL-2000;
                                                                                                                                                                                                                                                                                                                                            Tang YT,
Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         302
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                                                                                                                                                                                                                                                                                                                             The present sequence is given in the olism of a specification relating to a novel family of heta sub-unit protestis from a voltage-gated sodium channel; hamm and rat bette sub-units, which have been collectively identified as beta; have been isolated. The polymoleocides and polypeptides are useful for exceeding for agonistic and antegonists of sodium channels. The agonistic and antegonists of sodium channels. The agonistic and successing associated with voltage-gated sodium channels, e.g. pain, epilepsy, strock, isothermia, heart Glessee, cookeen gyndrome, Remliai Nondromeffin Paragangliama, Phenylecomiza and Charcom Remliai.
                                                                                                                 Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sedium channel, and their corresponding polypeptides, usefull for sedium treating sodium channel-associated conditions, e.g., pain, defecting and treating sodium channel-associated conditions, e.g., pain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 AIGCCIGCCTICAACAGAINGCTICCCCTAGCTICTCTAGTGCTCATCTACTGGGTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 536.6; DB 21; Length 2220;
Pred. No. 9.5e-137;
0; Mismatches 69; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2220 BP; 573 A; 557 C; 561 G; 529 T; 0 other;
                                                                                                                                                                                                                                                                    Claim 6; Page 69-70; 88pp; English.
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Matches 578; Conservative
                            2000-665241/64
                                                                                                                                                                                                                epilepsy and stroke
                                                             P-PSDB; AAB36001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GICTGCTTCCCTGTGTGTGTGTGTGTCCCTCGGAGACGGAGGCCGTGCAGGGCAACCCC
                                                                                                                                         ATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGAGGAGGTGGAGGCCACCACGACGTG
                                                                                                                                                                                        415 ATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAAGAAGAGGAGGCCACCACGGTGTG
                                                                                                                                                                                                                                                                    GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC
                                                                                                                                                                                                                                                                                                                   GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATTCGGAATGCC
                                                                                                                                                                                                                                                                                                                                                                                           CACCAGGAGGIGGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGGACGIGICCATCACGIGTCAACGICAACGAACGACTCTGGACGCCTCTACACCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGGACTTCACCTCTGTGGTCTCAGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    775 AIGAIGIACAICCITCIGGICITCCICACCIIGIGGCIGCICAICGAGAIGAIACAITGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGTCTGACTACC-TTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAGATGATATATTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCCCATCTGAGAACAAGGAGAACTCTGGGGTACCAGTGGAGGAA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGATTCCATTTGAGAACAGGGAAAATTCTTCGGTACCTGCGGGGGGA 941
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UNIV CAMBRIDGE TECH SERVICES LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morgan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC67836 standard; cDNA; 2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jackson A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-FEB-2000; 2000WO-EP01783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0129473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200063367-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-FEB-2001
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(UYCA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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422 120 482 542 602 300 662 360 722 420 782 480 540

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180 240 842

420 497 540

617

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421 ATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATC 480
                                                                                                                                                                                   198 ATACCTTTGCGAGTCACTGAAGAGGGGGGGAGAAGTCTTCACCTCCGTGGTCTCGGAAATC 557
                                                                                                                                                                                                                                                                                                                              TACADAAAGGTCTCAAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGTCTGACTACCTTGCC 600
                                                                                                                                                                                                                                                                                                                                                           378 CAGGACGTATCCATCACTGTACTCAATGTCACTTTGAATGACTCTGGCCTCTACACATGC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of the rate codium channel beal protein, designated Alras9465. This protein is involved in the generation of pain and other sensory or protein the paralleles in the generation of pain and endurance of mood, neutrodegenerative and sleep disorders, and in the control of mustle contraction, including any elegated paints as the term thear, dispession and vessular cone; The equinoses can be used in predictive medicine, screening and dispositio
                                                                                                                                                                                                                                                                558 ATGAIGTACATCTCCTGACTTCTCTCTGTGGCTGTTATTGAGATGATCTATTGC
                                                                                           438 AATGTGTCCAGGGAGTTCGAATTCGAGGCACACAGGCCTTTTGTGAAGACCACGAGACTG
                                               161 AATGIGICCCGGGAGTITGAGTTTGAGCCGCATCGCCCTTTGTGAAGACGACGCGGCTG
                                                                                                                                                                                                                                  ATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTCATCGAGATGATATATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New rat sodium channel beta-3 subunit gene isolated from a rat dorsal root ganglion CNR library for use in 'chromosode mapping, forensic medicine, monitoring clinical trials and therapeutics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; musçle contraction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 536.6; DB 22; Length 3108;
Pred. No. 1.1e-136;
0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat sodium channel beta3 protein Alrxa94h5 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          678 ATCCCTTCAGAGAACAAGGAGAACTCTGTGGTACCTGTGGAGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                      601 ATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3108 BP; 830 A; 748 C; 727 G; 803 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC90600 standard; cDNA; 3108 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MILL-) MILLENNIUM PHARM INC.
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Best Local Similarity 89.3
Matches 578; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattue sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the process and coding sequences of the rat scaling chains chain process and coding sequences of the procession of pain and chain chainsoy or procession is impulses. In the generation of pain and other sensory or preceptive merve impulses, in the establishment and endurance of mood, neurodeseneative and sleep discovers and an the control of muces contraction, including movements such as the heartbeat, dispession and vascular tone. The sequences can be used in predictive medicine, screening and diagnostic assays, and in pharmacoganomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New rat sodium channel beta-3 subunit gene isolated from a rat dorsal root agaglion cuba library for use in chromesome mapping, forensic medicine, monitoring clinical trials and therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTATCTACTGGGTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCTGCTTCCCTGTGTGTGTGGAAGTGCCCTCGGAGACAGAAAGCGGTGCAGGGCAATCCC
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                                                                                                                                                                                                                                                        Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder;
                                                                                                                                                                                                                                                                                  neurodegenerative disorder; mood disorder; muscle contraction; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; DB 22; Length 2632;
1e-136;
thes 69; Indels 0;
                                                                                                                                                                                                         sodium channel beta3 protein Alrxa94h5 related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2632 BP; 693 A; 636 C; 611 G; 692 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 536.6; DB; Pred. No. 1e-136
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1, Page 41-42; 145pp; English.
                                                                     AAC90602 standard; DNA; 2632 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 82.8%;
al Similarity 89.3%;
578; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-2000; 2000WO-US13144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0134198
                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                          WO200069912-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1999;
                                                                                                                                                                13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Curtis RAJ;
                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
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                                                                                        New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodysersity.
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Pred. No. 2.3e-136;
0; Mismatches 22; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                            Claim 1; SEQ ID No 22568; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.7%;
Matches 572; Conservative (
                    WPI; 2001-639362/73.
P-PSDB; ABG22577.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #22568.
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This sequence represents an expressed sequence teq (BEY) and is a polymuclectide of the invention are polymuclectides of the invention are polymuclectides of the invention are all secreted SEY sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to such the preventing or continties with would make them suitable for treating preventing or anellocating medical conditions in humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541 TACAGAAAGGTCTCTAAGGCCGAAGAGGCACACAGGAAAATGCGTCTGACTACCTTGCT 600
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                                    241 CACCAGGAAGTGGAGAGCCCCTTCCAAGGCCCGTCTGCAGTGGAATGGGAGCAAAGACCTG
                                                                               CAGGACGIGICCATCACTGIGCICAACGICACTGIGAACGACTCTGGCCTCTACACCTGC
                                                                                                                           101 CAGGACGIATCCATCACTGIACTCAATGICACTITGAATGACTCTGGCCTCTACACATGC
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Treacy M;
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Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-070076/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides the protein and coding sequences of the rat sodium channel bera3 protein (designated Alras946. This protein is involved in the generation of pain and other sensory or perceptive nerve inpulses, in the sexabilishment and enharance of mod, matrodepeneative and site persent so and site are are archaer, degestion and vascular content, including movements such as the heartbaer, degestion and vascular cone. The sequences can be used in predictive medicine, screening and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                    1003 TTGCTACAGACAGGTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGCCAAGAAAC 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                               537 TTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGTCTGACTAC
                                                                                                                                                                                                                                                                                                                                                                                         Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; muscle contraction; ss.
                                                                                                                                                                                                                                                                                                                                                 Rat sodium channel beta3 protein Alrxa94h5 partial coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          root ganglion cDNA library for use in chromosome mapping, forensic medicine, monitoring clinical trials and therapeutics -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.5%; Score 534.6; DB 22;
89.3%; Pred. No. 2.1e-136;
ive 0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 40-41; 145pp; English.
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                                                                                                                                                                                                           AAC90601 standard; cDNA; 645
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Matches 576; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-NOV-2000
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                                                                                                                                                                                                                                                      AAC90601;
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animals, altrough no supporting data is given. Suggested activities include nutritional activity, immune stimulating for suppressing activity, heatestopoisais regulating activity, tissue growth activity, heatestactic/chmoxinites activity, heatestact and thromolytic activity, receptor/ligand activity, and activity, activity, activity, receptor/ligand activity, and activity, and activity, and activity, and activity, and activity, and activity, and activity activity activity activity activity activity activity activity activity activity activity activity.
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                                                                                                                                                                                                                                                                                                                                                                 89 GTCTGCTTCCCTGTGTGTGTGTGCCCTCGGAGACGGA-GCCGTGCANGGCAACCCC
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                ;
                                                                                                                                                                                          Score 422; DB 20; Length 471;
Pred. No. 1.3e-105;
0; Mismatches 1; Indels 1
                                                                                                                                                         Seguence 471 BP; 93 A; 126 C; 143 G; 108 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #22567.
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                                                                                                                                                                                          65.1%;
99.5%;
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2000US-0649167.
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                                                                                                                                                                                                                             433; Conservative
                                                                                                                                                                                                          Local Similarity
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23-AUG-2000;
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                                                                                                                         therapy.
                                                                                                                                                                                            Query Match
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Matches
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The invention relates to isolated polynucleotide (I) and compared to the invention relates to isolated polynucleotide at in profession of polynucleotide and the recombination of isolated and for chromosome and gene mapping, and in recombination of isolated and for chromosome many decided and general disponsibility of the profession of the profession of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relationship of the relatio
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                                                                                                                                                                        New isolated polymorbectide and encoded polypectides, useful in adgranctide, forensice, gene mapping, identification of mitations responsible for genetic disorders or other traits and to assess biodylversity.
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Pred. No. 3.1e-97;
0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3531 BP; 952 A; 901 C; 960 G; 718 T; 0 other;
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                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID No 22567; 103pp; English.
                           Tang YT;
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Conservative
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                                                                                  WPI; 2001-639362/73.
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                           Drmanac RT,
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Matches 395;
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106 166 226 286 346 406

3250

3251 GCCTCTACACCTGCAATGTGTCCCCGGGAGTTTGAGGTTTGAGGCCCATCGGCCCTTTGTG 3310

407 AGACGACGCGCTGATCCCCCTAAGAGTCACCGAGGAGG 445

3311

ВР.

AAS86762 standard; cDNA; 621

RESULT 13

3349

347 GCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGA

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178 GACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGGTTTGAGGCGCATCGGCCC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GAGGAAGACGACGATTTGAGGGCCGCGTGGTGTGGAACGGCAGCCGGGGCACCAAGGAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ret sodium channal berås procekn, designated Airzassids. Bris procekn i sinvolved in the generation of pain and other sensory or perceptive nerve impulses, in the establishment and endurance of mod, neurodegenesative and allege disorders, and in the control of muscle contraction, including movements such as the heartheat, dispession and vascular room. The sequences can be used in predictive medicine, screening and dispussic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention provides the protein and coding sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 6 ATCTCCTGCATGAAGAGAGAGGGGGGGGGGGCCACGGTGGTGGAATGGTTCTACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 Arcrecideaacecececaceaaceaaceaceaceaceacacerreaceaaacerrecee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCGAGGGCGGTAAAGATT-----TCCTTATTTACGAGTATCGGAATGGCCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 GAGGTGGAGAGCCCCTTTCAGGGCGCCTGCAGTGGAATGGCAG------CAAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
root ganglion cDM ilbrary for use in obromosome mapping, forensic
medicine, monitoring clinical trials and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TGTGTGGAAGTGCCCTCGGAGACGGAGGCCGTGCAGGGCAACCCCATGAAGCTGCGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 recerceaegrecaecrecaagacecaagecercracegargacerreaaaarrereec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CAGAAGGGCACTGAGGAGTTCGTCAAGATCCTGCGCTATGAGAACGAGGTGCTGCAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat; sodium channel beta3 protein; Alrxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; muscle contraction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 148.2; DB 22; Length 657;
Pred. No. 1.4e-30;
0; Mismatches 223; Indels 21;
                                                        400 TITGIGAAGACGACGCCCCTGATCCCCCTAAGAGTCACCGAGGAGG 445
                                                                                                   238 TTTGTGAAGACGACGGGCTGATCCCCCTAAGAGTCACTGAGGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 657 BP; 146 A; 181 C; 213 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rabbit sodium channel betal protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure, Fig 5, 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assays, and in pharmacogenomics.
                                                                                                                                                                                                                                                                         AAC90603 standard; cDNA; 657 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0134198.
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                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        API; 2001-122743/13.
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                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curtis RAJ;
                                                                                                                                                                                                                                                                                                                                       AAC90603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196
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                                                                                                                                                                                                                RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynathocoties (1) and polynatics of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 ATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGGCCCCTTTCAGGGGCGCCTGCAG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAATGCCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAAC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 TGGAATGGCAGCAGCAGCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAAC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCC 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                           Human, chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polymucleotide and encoded polypeptides, useful in
adapostics, forensics, pene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                  DNA encoding novel human diagnostic protein #22566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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0; Mismatches 1;
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99.6%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 22566; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
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                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                   MO200175067-A2.
                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                          13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
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                                     AAS86762;
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                                          158 TGCAATGTGTCCCGGGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGG 417
                                                                                                                                                                                                                                                             418 CTGATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCAGAA 477
                                                                                                                                                                                                                                                                                                                                                                                                 478 ATCATGATGTACATCCTTCTGGTCTTCCTCACCTGTGGCTGCTCATCGAGATGATAT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                338 TGCTACAGAAAGGTCTCAAAAGCCGAAGAGCA---GCCCCAAGAAAACGCGTCTGACTAC 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541 TGCTACAAGAAGATCGCGGCCGCCACGGAGGCAGGAGGAGAAACGCCTCGGAATAC 600
CTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACC 357
                                                                                                                                                                                        recentrational description of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of the contration of t
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briege-gated sodium channel, useful for disponsing e.g. epilepsy, or
for screening modulators of sodium channel activity that may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sodium channel; mutation; epilepsy; anticonvulsant; mutant; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "voltage-gated sodium channel mutant
beta-1 subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human voltage-gated sodium channel mutant beta-1 subunit DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              595 CTTGCCATCCCATCTGAGAACAAGAGAACTCTGCGG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601 TTGGCCATCACTCAGAAAGCAAAGAAATTGCACGG 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
101..757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ23837 standard; DNA; 1414 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAY-2002; 2002WO-AU00581.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-2003 (first entry)
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The invention relates to an isolated nucleic acid molecule (mutDNA), that encodes a mutant mammalian beta-1 subunit (SCNIB) of a voltage-gated sodium channel, where a mutation event has occurred, which disrupts the functioning of an assemble sodium channel, to produce an apilepsy phenoxype. The mutation does not result in a Cl21% substitution in the

Claim 6; Page 45-47; S2pp; English.

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Mammalia, Eurheria, Primates, Catarrihini, Hominidae, Homo.
1. (bases 1 to 1201) Primates, catarrihini, Hominidae, Homo.
11, Ma. S. Gubber, C., Jessee, J. and Polayes, D.
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96.4%; Score 624.4; DB 13; Length 1201;
Best Local Similarity 98.8%; Pred. No. 3.6e-157;
Marche Gels, Conservative 3; Mismatches 4; Indels 1;
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venue Genoscope sequence
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1, .1201
                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                   mol type="mRNA"
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Matches 578; Conservative 0: Mismatches 69; Indelse 0; Gape 0; 1 ATGCCTCCTCAATAGATTGTTCCCCTGGTTCTCTGTGTTAATCAACTGGTCGTG 57 ATGCCTGCTTCAACAGATTGTTCCCCTGGTTCTTCTAACTACTCTAACTGGTCGAA 61 GTTCTCTTCCTCTGTGTGTGTGTGTGTGTTGTTGTTCTTAACTGGTTCAACTGGTCTCAACTGGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	237 decription de des des des des des des des des des	35 MINISTRACTOR CONSIDERATION OF THE PROPERTY OF THE PROPERTY OF A 20 412 MINISTRACTOR CONSIDERATION OF THE PROPERTY OF THE PR	541 TACAGAMAGSTETPANANGCCGANGAGGCGCCCAAGAMACGCGTTGACTTGCC 600 597 TACAGAMAGSTETTANGGCGGANGAGGGAGCTACGAGAMATACTCTTGTTTTTTTTTTTTTTT		JOURNAL Meth. Entrymol. 303, 19-44 (1999) JOHNAL SERVICE STATE High Character State

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| Core Eage="12 days embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cranslation="Mprivallelaslulliym" (vcpv) (vupseteavogansmila) cranslate ion="Mprivallelaslulliym" (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (vcpv) (
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89.3%; Pred. No. 2.8e-133;
iive 0; Mismatches 69; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="FANTOM DB:C530046B12"
/db xref="taxon:10090"
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                    URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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/strain="C57BL/63"
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Best Local Similarity 89.3
Matches 578; Conservative
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Bonaldo, Mr. J. Homoro, G. and Sozzee, M. B. Sozzee, M. S. Mormalization and subraction; two approaches to facilitate gene
                                                                             770 TAATGIGICTCCAGGGAGTTICAGTICGAAGCACACAGGCCCTTIGIGAAGACCACAAGACT 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 CTACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGTCTGACTACCTTGC 599
                                240 CCACCAGGAGGAGAGGCCCCTTTCAGGGGCCCTGCAGTGGAATGGCAGCAAGGACCT 299
                                                                                                                                                                                                                                                                                                                                                       360 CAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGCCT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 GAICCCCTAAGAGICACCGAGGAGGCIGGAGGACTICACCTCTGTGGTCTCAGAAAT 479
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OBN Library pepedaration. Dr. M. Bento Soares, Univeristy of Iowa
OBN Library Pepedaration. Dr. M. Bento Soares, Univeristy of Iowa
DNR Septencing Dy. Dr. M. Bento Soares, Universory of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BM933157
Uli-WrEH3-bag-d-O4-0-UL: IN UNI BMAP M.54 Mus musculus CDNA Clone
ULi-WrEH3-bag-d-O4-0-UIS', mRNA sequence.
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National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
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Fax: 301 443 9890
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                                                                                                                    SachMasson Alexana, Anternara, Anternara, Record, Carnincip, P., Mandania, S., Furuno, M., Hanagaki, T., Matera, H., Hanakatamas, W., Hayashida, S., Furuno, M., Hanagaki, T., Marca, M., Hanakatamas, W., Hayashida, S., Hyuten, M., Hanakata, H., Hanakata, M., Hanakata, M., Kadok, J., Kanakata, Y., Tabhi, Y., Itoh, M., Kagawa, I., Kanuikawa, T., Kanuikawa, T., Kanuikawa, T., Kanui, M., Kawa, J., Y., Koyiawa, Y., Godo, S., Komoni, H., Kowoni, H., Kowoda, M., Kanuika, M., Mandara, M., Mandara, M., Mandara, M., Mandara, M., Mandara, M., Mandara, M., Mandara, M., Mandara, M., Shanagawa, A., Balitaki, T., Sadanima, M., Sugabe, Y., Tagami, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M., Tagawa, M.,
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/strain="CSTBL/6J"
/db_xref="FaNYCM_DB:C330019103"
/db_xref="taxon:10090"
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Nature 420, 563-573 (2002)
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"Rifform integrated sequence analysis (RISBA) system-1984-former bees organisation planting with 1984 multicaphilary sequencer. Genome Res. 1961(11), 1751-1771 (2000)

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89.2%; Pred. No. 1.1e-126;
Live 0; Mismatches 67;
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Most maccular (Nouse control of Most maccular Bakaryota) Metacasa (Chordata, Cranlara, Vertebrata, Euteleoscomi, Mammilar Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (Bases 1 to 550) Missey, Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Most Chr. Phy (Mo
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cope, agape-remail.nh.gov
cobs. Library Preparation: Like Pennologies, Inc.
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DNA Sequencing Dy: Incyte Genomics, Inc.
Core distribution: NGC Colen distribution information can be
found through the I.M.A.G. E. Consortium/Libra at:
Found through the I.M.A.G. E. Consortium/Libra at:
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Beall: gegbbe-weall inhigo.
Tissue Procurement: Dr. Jam Lin, University of Iowa
cDN Library preparation: Dr. M. Bento Soarse, University of Iowa
ONN Library Preparation: Dr. M. Bento Soarse, University of Iowa
UNN Adparently Arrayed by: Dr. M. Bento Soarse, University of Iowa
ONN Library Arrayed by: Dr. M. Bento Soarse, University of Iowa
Clone Distribution: MGC clone distribution information can be
found though the I.M.A.G.B. Consortiuw/Librar at:
     481 ATGATGTACATCCTTCTTGGTCTTCCTCACCCTGTGGCTGCTCGAGATGATATTTGC 540
                                                                                                                                             This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA749111
01TH-FY0.-cdd-K-17-0-UI.FI WHE WARP, FY0 Wus musculus CDNA clone
18AGE: 6811594 5', mRNA sequence.
                                                                                                                                                                                                                                      541 TACAGAAAGGICTCAAAAGCCGAAGAGGCAGCAAGAAAAGGCGICTGACTA 596
                                                                                                                                                                                                                                                                                          626 TACAGAAAGGICICICTAAGGCCGAAGAGGCAG-1CAGGAAAAIGCGICTGACTACTI 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 1; Gaps
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.2e-109;
0; Mismatches 59;
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179 c 201 g
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Location/Qualifiers
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/strain="C57BL/6"
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Best Local Similarity 89.2%;
Matches 494; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 723)
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Source

FEATURES

BASE COUNT

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B0745919 box-d-18-0-UI.rN NH BAAP_EXO Mus musculus CBN clone
INGRESS 703781 5', mRNA sequence.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 408.4; DB 13; Length 927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61; Indels
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0; Mismatches 61
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Contact: Robert Strausberg, Ph.D.
'clone="IMAGE:6308278"
                                                                                                                                                                                                                                                                   is a NIH MGC Library.
                                                                                                                                                                                                                                                                                                         258 9
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Best Local Similarity 88.2%;
Matches 47%; Conservative
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TITLE
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menii capther-Genali Inhigor.

Tissue Procurement: Dr. Jasse Lin, Univeristy of Iowe CDN Library preparation: W. Bento Soarse, University of Iowe CDN Library preparation: Dr. W. Bento Soarse, University of Iowe DNN Library Arrayed Wr. Dr. W. Bento Soarse, University of Iowe DNN Edgementing by Dr. M. Pento Soarse, University of Iowe Chose Distribution: MCC close distribution; MCC close distribution; and on be
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T. Dasses 1C 1069, MR-RGG, cnc.nih.gov, MR-RGC Thep.//RGG, cnc.nih.gov, MR-RGC Thep.//RGG, cnc.nih.gov, MR-RGC Thep.//RGG, cnc.nih.gov, MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC MR-RGC M
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                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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N1H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BU118914 BST 25-NOV-2002 603142291F1 CSEQCHL16 Gallus gallus cDNA clone ChEST135F23 5', mRNA
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87.6%; Pred. No. 1.9e-85;
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                                                                                 organism="Mus musculus"
                                                                                                                                                                   'clone="IMAGE: 6847679"
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Matches 389; Conservative
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      Tull-length clones and was constructed by C. Gruber (Invircopan). Research Genetics tracking code 017. Note: this is a NIH MCC Library."
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071 AFFO-cfc-1-22-6-UL:XI NIE BAAPEFFO Mus musculus CDNA Clone
IMAGE: 6817879 5', mRNA sequence.
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Tissue Procurement: Dr. Jim Lin, University of Iowa CDM Likrary preparation In. M. Bento Source Mirwesticy of Iowa CDM Likrary preparation In. M. Bento Source Mirwesticy of Iowa DNA Sequencing Py. Dr. M. Bento Source, University of Iowa Clone Distribution Entribution Information can be found at http://gennem.lidoc.com/distribution information can be found at this offorce was contributed by the Brain Molecular Anatomy Perject
                                                                                                                                                                                                                                                                                                                   61 GICTGCTTCCCTGTGTGTGTGTGCCCTCGGAGACGGCGAGGCCGTGCAGGCAACCCC 120
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Library is normalized and enriched for
                                                                                                                                                  57.2%; Score 370.4; DB 12; Length 1069;
                                                                                                                                                                   Pred, No. 9.1e-89;
0; Mismatches 46; Indels
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Matches 434; Conservative
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Boardman, P. 8., Sanz-Ezquerro, J., Overton, I. M., Burt, D. W., Bosch, E., Fong, W. T., Tickle, C., Eroen, M. A., Wilson, S. A. and Hubbard, S. J. Curr. Biol. 12 (22), 1965-1969 (2002)
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University of Manchester Institute of Science and Technology (UMIST
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Archosauria; Aves Neognathae; Galliformes; Phasianidae;
Phasianiae; Gallus
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Pred. No. 1.5e-83;
0; Mismatches 145; Indels
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/mol_type="mRNA"
/mol_txain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST135£23"
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Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
            BU118914
BU118914.1 GI:25327626
                                                                                                              Gallus gallus (chicken)
Gallus gallus
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES Description	US-09-385-028-20 Sequence 20, Appl US-09-726-614-20 Sequence 20, Appl	Sequence		US-09-365-028-1 Sequence 1, Appli US-09-726-614-1 Sequence 1, Appli	88 Sequence	Sequence	3 Sequence 3363,	311 Sequence 3311	Sequence 2	Seguence 1	322 Sequence 3322	Sequence	31,	37,	Seguence 52,	2593	2325 Sequence 232	Sequence	Sequence 1,	-09-911-176B-1 Sequence 1, App	Seguence 1,	Sequence 1, Ap	US-09-252-991A-2512 Seguence 2512, Ap	9, Ap	-08-885-418-9 Seguence 9, Appli
SUM	US-09-3	US-09-3	08-09-	US-09-30	60-SD	US-09-4	US-09-2	US-09-2	US-09-6	DS-09-4	-60-SD	-60-SD	-60-SD	-60-SD	-60-Sn	US-09-	60-SD	US-09-1	-60-SD	-60-SD	-60-Sn	-60-SD	-60-SD	US-08-	-80-SD
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Query Match Best Local Similarity

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APPLICANT: Susemen A. Aidoo
APPLICANT: Ashish S. Paradkar
APPLICANT: Ashish S. Paradkar
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Petent No. 6514735
TITLE OF INVENTION: DIA Sequence Encoding Enzymes of Clavulanic
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STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
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RECISTRATION WIMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECHMONILATION INFORMATION:
TELEPHONE: (202 638-6666
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PRIOR PAPLICATION DATA:
APPLICATION NOMBER: US 08/790,462
FILING DATE: 29-AM-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/09/726,614
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IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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Patent No. 6514735
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RCA 248593 IDEA UR
FOR SEQ ID NO: 20:
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Matches 109, Conservative
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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APPLICANT: Susan I
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Washington
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OPERATING SYSTEM: PC.DOS/MS.DOS
SOFWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
FILMN DATE:
CLASSING DATE:
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NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
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FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
Sequence 13, Application US/09385028
Patent No. 6232106
                                                                                                                                                                                                                                                      APPLICANT: Sugan E. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Anish S. Paradkar
TITLE OF INVENTION: DNA Sequer
Patent No. 6322106
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REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 14,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 638-6666
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INFORMATION FOR SEQ ID NO: 13:
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Best Local Similarity 47.4%;
Matches 109; Conservative (
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Appirown: Sussen E. Jensen
Appirown: Assan A. Nardkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent W. 63210AC TO AND Sequence Encoding Enzymes of Clavulanic
RITLE OF INVENTION: Acid Biocoputhesis
NUMBER OF SEQUENCES: 25
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IBM PC compatible
VSTERM: PC-DOS/MS-DS
PatentIn Release #1.0, Version #1.30 (EPO)
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ATTORNEY/AGRY IRRORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24.514
REFERENCE/DOCKET NUMBER: 1118/P57452US2
TRILCOOMANNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
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APPLICATION NUMBER: US/09/385,028
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Patent No. 6232106
GENERAL INFORMATION:
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TELERAX: RCA 42665
TELERAX: RCA 42693 IDBA UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15079 base pairs
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC comp
OPERATING SYSTEM: PC
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COUNTRY: U.S.A.
ZIP: 20004
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F: The Jenifer Buliding, 400 Seventh Street, N.M.
Washington
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OFFERTING SYSTEM: PC DOS/MAS.DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRANT APPLICATION NATR:
CAPALLCATION NUMBER: US/09/726,614
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APPLICATION DATA:
APPLICATION WREBE: 19.08/790,462
ALTOHON DATE: 29.73M-1997
ATTOHON DATE: 19.73M-1997
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REGISTRATION NUMBER: 34.514
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TELEPHONE: (202 3340556
TELER: NCA 44853 IDBA UR
INFORMATION FOR SEQ ID NO: 13:
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MOLECULE TYPE: DNA (genomic)
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US-09-726-614-13
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APPLICANT: Zhang, Zemin
ITTLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
                                         10470 CGCCCGGGTCGGCATCGAGGCGGAGGTGCTGGACTTCCCGTCGGCGACT 10519
423 CCCCCTAAGAGTCACCGAGGAGGCTGGAGGACTTCACCTCTGTGGTCT 472
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CURRENT PELING DATE 1200.11.14

RECOR PELING DATE: 200.11.14

PRIOR PELING DATE: 300.10.14

RECOR APPLICATION WINBER: 60/04987

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RECOR APPLICATION WINBER: 60/04987

RECOR PELING DATE: 1399-10.1

RECOR PELING DATE: 1399-10.1

RECOR PELING DATE: 1399-11.1

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FPILING DATE: 1998-03-20
R PELING DATE: 1998-04-28
R FEDELICATION NUMBERS: 66/084600
R FILING DATE: 1998-05-07
R RAPLICATION NUMBERS: 66/087106
R FILING DATE: 1998-05-07
                                                                                                                                                                                                                               Sequence 388, Application US/09996243
Fatent No. 6478825
GENERAL INFORMATION:
APPLICANT: ASINEMAZI, NVi J.
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FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/087827
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
FILING DATE: 1998-06-04
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
Wood, William I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
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                                                                                                                                                                                                                                                                                                                                                                 Baker, Kevin P.
Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Goddard, Audrey
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                                                                                             10470 ceccessresecarceacarceasesesecresacriceercerceacac 10519
                                                                                                                                                                                                                                                                                                                                                                 423 CCCCCTAAGAGTCACCGAGGAGGCTGGAGAGTTCACCTCTGTGTGTCT 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSES: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Sevench Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFWARE: PatentIn Release #1.0, Version #1.30 (BPO) CURRENT APPLICATION DATA:

USA PELICATION STATE US/09/726,614
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US-09-726-614-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS PETICE
REGISTRATION NUMBER: 24,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              Sequence 1, Application US/09726614
Patent No. 6514735
GENERAL INFORMATION:
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TELECOMMUNICATION TOORWATION:
TELEFONE: (202 389 656
TELEFONE: (202 389 5350
TELEFONE: RCA 248591 IDEA UR
INPORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS.
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nucleic acid
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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: U.S.A.
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HYPOTHETICAL: NO
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US-09-726-614-1
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NR APELICATION NUMBER 60/088742
FILING DATE: 1998-06-10
OR APELICATION NUMBER: 60/08810
FILING DATE: 1998-06-10
SR APELICATION NUMBER: 60/08824
SR APELICATION NUMBER: 60/08824
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RAPETATORAM MARE "(6/109563
RAPETATORAM WRIGHS (6/109563
RAPETATORAM WRIGHS (6/109561
RAPETATORAM WRIGHS (6/109501
RAPETATORAM WRIGHS (6/109507
RAPETATORAM WRIGHS (6/109507
RAPETATORAM WRIGHS (6/109508)
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 66/08612
PELLINS DATE: 1988-06-05
APPLICATION NUMBER: 66/08617
PELLINS DATE: 1988-06-05
APPLICATION NUMBER: 66/08665
PELLINS DATE: 1938-06-09
APPLICATION NUMBER: 66/08613
PELLINS DATE: 1938-06-10
APPLICATION NUMBER: 66/086138
R FILING DATE: 1398-06-04
R FILING DATE: 1398-06-04
R FLING DATE: 1398-06-07
R PAPLICATION NUMBER: 60/08030
R FLING DATE: 1998-06-07
R FLING DATE: 1998-06-07
R FLING DATE: 1998-06-07
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PLICATION NUMBER: 60/08326
LING DATE: 1998-066-04
LING DATE: 1998-06-05
LING DATE: 1998-06-05
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LING DATE: 1998-06-05
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RRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
RRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
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FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088858
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PLICATION NUMBER: 60/089105
LING DATE: 1998-06-12
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PPLICATION NUMBER: 60/089532
ILING DATE: 1998-06-17
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LICATION NUMBER: 60/089598
LICATION NUMBER: 60/089599
LICATION NUMBER: 60/089599
ING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/089948
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LICATION NUMBER: 60/08861
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FILING DATE: 1998-06-16
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LICATION NUMBER: 60/089514
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Matches 95; Conservative
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TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ALGORISM FOR DIAGNOSTICS AND FHERAPEUTICS
CURRENT PLILAY DALLOCATION NUMBER: US 60/094,190
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Patent No. 6551793 3111. Application US/09252991A
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APPLICATION INDMER: PCT/GB98/01294
FILING DATE: 06-M9X-1398
APPLICATION INDMER: GB 709421.3
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: EMERY, Stephen Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
WHORER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPANYING SYSTEM, PC-COMPANTIBLE
OPERATING SYSTEM, PC-LOGS/MS-DOG
SOFTWARE: NS WORL
CURRENT APPLICATION BOWNERS: US, 09/422, 439
FILLING DIEE: 09-NO 6339970-1999
CLASSIFICATION NUMBER: CHANDOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78-09-252-991A-3363
; Sequence 3363, Application US/09252991A
; Patent No. 6551795
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APPLICANT: Marc J. Rubenfield et al.
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ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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Best Local Similarity 52.33
Matches 79; Conservative
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MEPLICANT: MARC 3, RADERLEGAD GE 20, ANINO ACID SEQUENCES RELATING TO PSEUDOWONAS TITLE OF INTERTOR. MICHERIC ACID AND ACID SEQUENCES RELATING TO PSEUDOWONAS TITLE OF INTERTOR. MACHINE ACID AND THERAPEUTICS.

FILE REPRESENCE: 1.0156.136
CURRENT FELLING DATE: 1999-02-18
FRICA REPLICATION NUMBER: US 60/074,788
FRICA REPLICATION NUMBER: US 60/094,190
FRICA RELICATION NUMBER: 1999-02-18
FRICA RELICATION NUMBER: US 60/094,190
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FRICA RELICATION NUMBER: US 60/094,190
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Matches 79; Conservative 0; Mismatches 72; Indels
                                                                                                                                                                                            NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
SIREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1587 deregaagegegegegegegegaagerig 1617
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APPLICATION INVERS: PCT/GBSE/01294
FILING DATE: 05-8AY-1598
APPLICATION REMEST: 68 970442.3
FILING DATE: 10-8AY-1597
INFORMATION FOR SEQ. ID NO. 15:
SEQUENCE CHARACTERISTICS:
                                                                                                              APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS Word
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*** NOLECTUR TYPE: other mucleic acid
US-09-423-439-15
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: <Unknown>
                       Sequence 15, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                         Washington
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    US-09-423-439-15
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1031 TGTCGATCCCGACCCTCGGCGCAGCGGTTTCGGCTACCAGGTGGCGCGAGTTCGGCC 972
                                                       245 AGGAGGTGGAGAGCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTGCAGG 304
                                                                                                              971 AcéAddriccriccGACCGCGCCCCGGGCTGCTGCTTCACCATCACCGACCAGTTGAAGG 912
                                                                                                                                                                     305 ACGIGICCATCACTGIGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGCAATG 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillebury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1584 GCTGGAAGAGCGCGCGCAGAGAAGAAGCTG 1614
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APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-M9X-1999
APELING DATE: 05-M9X-1999
APELING DATE: 10-M9X-1997
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
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COMPUTER READABLE FORM:
MEDIJW TYRE: Floppy disk
COMPUTER: IS IN PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: NS WORD
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MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
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Patent No. 6339070
GENERAL INFORMATION:
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STRANDEDNESS: single
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US-09-423-439-25
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RESULT 12

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1557 GCGCTTCCAGTGGACCATCGCCAAGGCCGGGTCTCGAACATCATCCCCGCCAGCGC 1616
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          270 gcgccrgcharganargechagancargchagancargargarchacargargargar 329
                                                                                                 330 CACTCTGAACGACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 CACTCTGAACGACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTTGAGGC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 5.5%; Score 35.8; DB 4; Length 2019; 1.5imilarity 52.3%; Preda No. 2.1; children 27; Conservative 0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUMBER OF SEQUENCES: 60
CORRESSONDENCE ADDRESS:
STREEF: 1100 Wew York Ave., N.W.
CITT: Maghington
                                                                                                                                                                                                                     1656 GCTGGAAGAGGGGGGGCAGCAGAAGAAGCTG 1686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1677 GCTGGAAGAGCGCGCGCAGCAGAAGAAGCTG 1707
                                                                                                                                                                                         390 GCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 GCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/GB98/01294
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: No WORD
CHRRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 05-No. 639070-1999
CLASSIFICATION: «UDRIDOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 02-MAY-1938
APPLICATION WHER: GB 9709421.3
INFORMATION FOR SEQ. IN NO. 31:
5ROURING CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: December 5, 2003, 22:59:15
                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2019 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Job time : 58.0404 secs
                                                                                                                                                                                                                                                                                                                              US-09-423-439-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-423-439-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
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                                                                                                                                                                                         125 AGCTGCGCTGCATCTCCTGCATGAAGAGAAGAGGTGGAGGCCACCACGGTGGTGGAAT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 ACGTGTCCATCACTGTGCTCAACGTCACACTCTGAACGACTCTGGGCCTCTACACCTGCAATG 364
                                                                                                                                                                                                                                   438 Accindentaceaceaceacasanarecerración actracionareceración de Astronomia 437
                                                                                                                                                                                                                                                                                185 GGTTCTACAGGCCCCGAGGCCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGCCACC 244
                                                                                                                                                                                                                                                                                                                          498 TGTCGATCCGACCCTCGGCCCCACCGGTTCGGCTACCAGGTGGCGCGCCCAGTTCGGCC 557
                                                                                                                                                                                                                                                                                                                                                                 558 ACGAGGTGCTGCCGACCCGCCGGCCGGGCTGCCGTTCACCATCACCGACCAGTTGAAGG 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  618 AGCTGTGTGCCGAGCTTTCCGGCACCTCGTGGATTGCCGGGTGAGCTGCAACGGCCAAG
                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.5%; Score 35.8; DB 4; Length 1998; Bet Local Similarity 52.3%; Pred. No. 2.1; Matches 79; Conservative 0; Mismatches 72; Indels 0;
                                                                                                 5.5%; Score 35.8; DB 4; Length 1995; 45.8%; Pred. No. 2.1; tive 0; Mismatches 147; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 TGTCCCGGGAGTTTGAGTTTGAGCGCGCATCG 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      678 retrecededaacerecterreacecates 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APRIZORYTON DAPA. M. PERIOR APPLICATION NUMBER: PCT/G898/01294 FILTING DATE: 0.5-MAY-1398 APRIL ATTON NUMBER: G8 709421.3 INFORMATION NUMBER: 0.5-MAY-1397 PLAING DATE: 1.0-MAY-1397 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: 'R Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 633970-33439
FILLING DRIE: 09-No. 63970-3999
CLASSIFICATION: CHIKNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IEM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY lines MULEULE TYPE CENER BESCRIPTION: SEQ ID NO: 50: 08-09-423-439-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1998 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                    TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                     Query Match
Best Local Similarity 45.8%
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
                                             , ORGANISM: Pseudo
US-09-252-991A-3322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-423-439-50
LENGTH: 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
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Copyright (0) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 5, 2003, 17:39:02; Search time 269.786 Seconds (without alignments)

Title: US-09-936-680-4_COPY_376_1023

Perfect score: 648
Sequence: 1 atgeorgcettcaatagatt.........cggtaccagtggaggaatag 648
Scoring table: Insperiry US-09.00, Gapext 1.0
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	4403344		
Searched: 2201672 segs, 1661799599 residues	Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100%

Partinime of heart Surport	1	
	Database :	

Pred. No. is the number of results predicted by chance to have a sorre greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					0777		_
Result No.	Score	Query	Query Match Length DB	80	ΩI	Description	
-	648	100.0	1361	ន	US-09-997-579-4	Sequence 4, Appli	
8	536.6	82.8	2220	10	US-09-997-579-3	Seguence 3, Appli	_
m	536.6	82.8	2632	13	US-10-029-191-22	Sequence 22, Appl	_
4	536.6	82.8	3108	33	US-10-029-191-1	-i	_
S	534.6	82.5	645	13	US-10-029-191-21	Sequence 21, Appl	-
φ	148.2	22.9	657	13	US-10-029-191-23	Sequence 23, Appl	-
7	138.6	21.4	1490	9	US-09-917-800A-1654	Sequence 1654, Ap	_
80	49	7.6	243	25	US-10-029-386-16214	Sequence 16214. A	
6	49	7.6		12	US-10-029-386-2514	Seguence 2514, Ap	
10	39.2	6.0		175	US-10-094-466-63	Sequence 63. Appl	_
11	39.5	6.0		75	US-10-120-988-120	Secuence 120, App	-
12	38.6	6.0		ø	US-09-815-242-7698	Seguence 7698, Ap	
13	38	6.0		15	US-10-102-622-9	Sequence 9, Appli	_
14	38	6.9		12	US-10-102-622-11	Sequence 11, Appl	_
c 15	37.4	5.8		175	US-10-311-455-912	Seguence 912, App	
16	37	5.7		σ	US-09-768-826-27	Sequence 27, Appl	

, Ap	App	Appl	App1	Appli	Appl	1, A	App	App	App	App	App	App	App	App														
5449,	517,	50,	13,	ä	44,	20831,	111,	388,					388,	388,	388,	388,	388,	388,	388,	388,	388,	388,		٠,	388,	388,	388,	388,
Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence 388	Sequence	Seguence	Sequence 388,	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-764-891-5449	US-10-205-428-517	US-10-458-201-20	US-10-458-201-13	US-10-458-201-1	US-10-101-510-44	US-09-918-995-20831	US-10-176-847-111	US-09-989-722-388	US-09-989-723-388	US-09-989-279-388	US-09-989-727-388	US-09-989-731-388	US-09-989-732-388	US-09-991-073-388	US-09-990-442-388	US-09-991-163-388	US-09-993-604-388	US-09-990-456-388	US-09-989-721-388	US-09-992-598-388	US-09-989-293A-388	US-09-989-735-388	US-09-990-444-388	US-09-991-181-388	US-09-989-730-388	US-09-990-436-388	US-09-993-687-388	US-09-989-734-388
H	14	12	12	12	12	11	14	σ	6	0	0	30	10	70	2	9	10	10	9	10	10	10	10	97	10	2	10	7
1548	1548	1668	11604	15120	250	451	673	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371	1371
5.6	9.6	5.6	9.9	5.6	5.6	9.6	9.6	9.6	5.6	5.6	5.6	9,5	5,6	5.6	2.6	2.6	5.6	5	9.6	9.5	5.6	5.6	5.6	9.9	9.0	9,6	9.6	2.6
36.6	36.6	36.4	36.4	36.4	36.2	36.2	36.2	36.2	36.2	36,2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2	36.2
c 17	c 18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 US-09-997-579-4

US-09-997-579-4	
; Sequence 4, Application US/09997579 ; Patent No. US20020113203A1	
; GENERAL INFORMATION: ; APPLICANT: Cambridge University Technical Services	1 Services
~	ta sub-unit proteins from a voltage gated s
, TITLE OF INVENTION: channel	
; TITLE OF INVENTION: nucleic acids encoding them and therapeutic or diagnostic uses	ing them and therapeutic or diagnostic uses
File KEFEKENCE: 6/4555-2001	ď
CHERENT FILTER DATE: 2002-04-05	
PRIOR APPLICATION NUMBER: PCT/BP00/01783	
PRIOR FILING DATE: 2000-02-24	
PRIOR APPLICATION NUMBER: 60,129,473	
; PRIOR FILING DATE: 2000-02-24	
; NUMBER OF SEQ ID NOS; 47	
, SOFTWARE: Patentin version 3.1	
SEQ ID NO 4	
; LENGTH: 1261	
; TYPE: DNA	
; ORGANISM: Homo sapiens US-09-997-579-4	
Query Match 100.0%; Score 648; Best Local Similarity 100.0%; Pred. No. 2.	Score 648; DB 10; Length 1261; Pred. No. 2.2e-197;
tive 0	ches 0; Indels 0; Gaps 0;
Qy 1 AIGCCIGCCTICAATAGATIGTTTCCCCIGGCTTCTCTCGGGTTATCTACTGGGGTCAGT 60	GGCTTCTCTCGTGCTTATCTACTGGGTCAGT 60
Db 376 AIGCCIGCCITCAAIAGAITGIIICCCCIGGCIICICCICGIGCIIAICIACIGGGICAGI	GGCTTCTCTCGGGCTTATCTACTGGGTCAGT 435
Qy 61 GTCTGCTTGCCTGTGGAAGTGCCCTCGGAGGCGGGGGCCGTGCAGGGCAACCCC 120	CTOGGAGAGCOGTGCAGGCAACCCC 120
Db 436 GFCFGCTFCCTGFGTGTGTGTGTGTGTGTGTGTGTGTGTG	CTCGGAGACGCCGTGCAGGCAACCCC 495
Qy 121 ATGAAGCTGCGCTGCATCTCCTCCATGAAGAGAGAGGAGGGCACCACCACGCGGGTG 180	GAGAGGAGGTGGACCACCACGGTGGTG 180
Db 496 ATGRACCTGCCTGCATCTCCTGCATGAAGAGAGAGAGGAGGAGGCCACCACGGTGGTG 555	GAGAGAGGAGGAGGCACCACGGGGGTG 555

722

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195-10-029-191-22
196-10-029-191-22
196-10-029-191-22
196-10-029-191-22
196-10-029-191-22
196-10-029-191-22
197-10-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029-191-029
181 GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 240
                                          241 CACCAGARGEGGAGGCCCTTTCAGGGGGCCTCCAGTGGAATGGCAGAAGGACCTG 300
                                                                                                                                                                        603 CACCAGGAAGTGGAGAGCCCCTTCCAAGGCCGTCTGCAGTGGAATGGGAGCAAAGACCTG 662
                                                                                                                                                                                                                                    301 CAGGACGIGICCATCACTGIGCTCPACGICACTCTGAACGACTCTGGCCTCTACACCTGC 360
                                                                                                                                                                                                                                                                                                                                                     361 AATGTGTCCCGGGAGTTTGAGGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACGCGGCTG 420
                                                                                                                                                                                                                                                                                                                                                                                                        723 AATGTGTCCAGGGGTTCGAATTCGAGGCACACAGGCTTTTGTGAAGACCACGAGACTG 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 ATCCCCTAAGAGTCACCGAGAGGCTGGAGAGCTTCACCTCTGTGGTCTCAGAAATC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 ATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAGATGATATATTGC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 TACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAACGCGTCTGACTACCTTGCC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 AIGCCTGCCTTCAACAGATIGCTTCCCCTAGCTTCTCTAGIGCTCATCTACTAGGGTCAGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CICIGCITCCCIGIGIGIGIGIGAGIGCCCTCGGAGACGGAGGCCGIGCAGGCAACCCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 GTCTGCTTCCCTGTGTGTGTGTGTGTGCCCTCGGAGAACAGAAGCGGTGCAGGGCAATCCC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAGGAGGTGGAGGCCCACCACGGTGGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ANGCONGCOTTCAATAGATTGTTTCCCCTGGCTTCTCCTCGTGCTTATCTACTGGGTCAGT 60
                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 82.8%; Score 536.6; DB 13; Length 2632;
Best Local Similarity 89.3%; Pred No. 17.9-161;
Matches 518, Conservative D; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      963 ATCCCTTCAGAGAACAAGGAGAACTCTGTGGTACCTGTGGAGGAATA 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601 ATCCCATCTCAGAACAAGGAGAACTCTGCGGTACCAGTGGAAGAATA 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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ORGANISM: Rattus sp.
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109-10-20-191-21
Sequence 21, Application US/10029191
Sequence 21, Application US/10029191
Sequence 21, Application No. UC20021060453A1
SEXEMAL INFORMATION: ROWA AJ.
TITLE OF INVENTION: ROWALY,
TITLE OF INVENTION: REACTER,
TITLE OF INVENTION: REACTER,
CURRENT APPLICATION NUMBER: 1910/02X/5UJ
CURRENT APPLICATION NUMBER: 09569, 970
PRIOR PRILING DATE: 2000-05-12
PRIOR PRILING DATE: 2000-05-12
PRIOR PRILING DATE: 1999-05-14
NUMBER OF SEQ. IN NOSE: 23
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Best Local Similarity 89.3%; Pred. Nismatches 59; Indels 0; Gaps
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FRICK REPLICATION NORSE: US/10/29/20/19
FRICK REPLICATION NORSE: US (6/134,198
FRICK PILIAR DATE: 200-05-12-6
FRICK REPLICATION NORSE: US (6/134,198
FRICK PILIAR DATE: 199-05-14
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                                                 CAGGACGIGICCATCACTGIGCTCAACGICACTCIGAACGACTCTGGCCTCTACACCTGC 360
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          181 GAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGGAATGGC 240
                                                                                                                                             241 CACCAGGAGGTGGAGGCCCCTTTCAGGGCGCCTGCAGTGGAATGGCAGCAAGGACCTG 300
                                                                                                                                                                                                         318 CACCAGGAAGTGGAGAGCCCCTTCCAAGGCCGTCTGCAGTGGAATGGGAGCAAAGACCTG 377
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89.3%; Pred. NO. 1.88-16;; Indels 0; Gaps
tive 0; Wismatches 69; Indels 0; Gaps
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Best Local Similarity 89.34
Matches 578; Conservative
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ORGANISM: Rattus sp.
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                  298 CIGCAGGACGIGICCAICACIGIGCICAACGICACICIGAACGACICIGGCCICIACACC 357
                                                                       301 CTGCAGGACCTGTCCATCTTCACCAATGTCACCTACAACCACTCGGGCGACTACCAG 360
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                                                                                                                                                                                                                                                                                                                                                                             478 ATCATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGAGATGATATAT 537
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US-09-917-800A-1654
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TITTE OF INVENTION MAINTENANCE OF MODELING
TOTRERY FLINED MATER: 2001-07-31
CURRENY FLINED MATER: 2001-07-31
CURRENY FLINED MATER: 2001-07-31
CURRENY FLINED MATER: 2001-07-31
CREATED APPLICATION NUMBER: US 60/222.040
PRIOR APPLICATION NUMBER: US 60/222.040
PRIOR APPLICATION NUMBER: US 60/222.040
PRIOR PAPLICATION NUMBER: US 60/222.346
PRIOR PAPLICATION NUMBER: US 60/222.336
PRIOR PAPLICATION NUMBER: US 60/222.336
PRIOR PAPLICATION NUMBER: US 60/225.336
PRIOR PALLON NUMBER: US 60/225.736
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; Patent No. US20020119462A1
; GENERAL INFORMATION:
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Castle, Arthur
Elashoff, Michael
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ORGANISM: Rattus norvegicus
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SOFTWARE: Patentin Ver. 2.1
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                                                    241 CACCAGGAAGTGGAGAGCCCCTTCCAAGGCGTCTGCAGTGGAATGGGAGCAAGAACTG
                                                                                                                                                                     301 CAGGACGTGTCCATCATGTGCTCAACGTCACTCTGAACGACTCTGGCCTCTACACCTGC 360
181 GAGTGGTTCTACAGGCCTGAGGGCGGTAAAGATTTCCTTATATATGAGTATCGGAATGGC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 23, Application US/10029191; Publication No. US20020160453A1; GERREAL INFORMATION: APPLICANT: CURTIS, Rory A.J.
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US-10-094-466-63
; Sequence 63, Application US/10094466
; Publication No. US20030203363A1
; GENERAL INFORMATION:
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Matches 104; Conservative
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US-10-029-386-2514
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APPLICANT Feath, Sharron G.
APPLICANT: Read, David K.
APPLICANT: Read, David K.
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OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | ANY OWNERFORM | 
Ouery Match 7,6%; Score 49; DB 12; Length 243; DB 55 Local Similarity 60.1%; Pred. No. 2.3e-06; Matches 104; Conservative 0; Mismatches 60; Indels Matches 104; Conservative 0; Mismatches 60; Indels
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Score 49; DB 12; Length 569; 60.1%; Pred. No. 3.2e-05; ive 0; Mismatches 60; Indels
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LENGTH: 569
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Sequence 7698, Application US/09815242
Patent No. US20020061569A1
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APPLICANT: HASELBECK, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2658 ACTGAACAACGC 2669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KRY: CDS
LOCATION: (49),.(4890)
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APPLICANT: SOVER 48. 1. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, P. 1970, 
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Bost Local Similarity 47.2%; Petch No. 0.11; 
Matches 119; Conservative 0; Wiemstches 133; Indels 0;
                                                                                                                                                                                                                                                                                                                                                         , Sequence 120, Application US/10120988
; Publication No. US20030219745A1
; GENERAL INFORMATION;
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APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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; LOCATION: (27)..(5961)
US-10-094-466-63
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LENGTH: 5973
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2418 GCACAAGGAGCTCGGGGAGGGCACGCTGACCTGCTGAAGCGCCAAGGCGGAGCTGGAGGA 2477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Owery Match 6.0%; Score 39.2; DB 12; Fength 6202; Ber Local Similarity 47.3%; Pred. No. 0.11; Metches 119; Oonservalive 0; Mismarches 133; Indels 0;
APPLICANT: Obliden, Kari L.
APPLICANT: Obliden, Kari L.
APPLICANT: Parkind, Judith W.
APPLICANT: Travick, Judith W.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, John D.
APPLICANT: Travick, Select T.
APPLICANT: Tamanary Robert T.
APPLICANT: Tamanary M. Boward
TITLE OF INTERPITOR I Deferification of Essential Genes in TITLE OF INTERPITOR : Provastyces
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CURRENT PRELICATION WURBER: 60/199/815,242

CURRENT PELICATION WURBER: 60/190/9615,242

CURRENT PILING DATE: 2001-03-21

PRIOR PELICATION WURBER: 60/190/80

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PELICATION WURBER: 60/200/348

PRIOR FILING DATE: 2000-05-23

PRIOR PELICATION WURBER: 60/201/727

PRIOR PELICATION WURBER: 60/201/727

PRIOR PELICATION WURBER: 60/201/727

PRIOR PELICATION WURBER: 60/201/727

PRIOR PELICATION WURBER: 60/201/737

PRIOR PELICATION WURBER: 60/201/737

PRIOR PELICATION WURBER: 60/201/737

PRIOR PELICATION WURBER: 60/201/737
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455 ACTICACCICIGIGGICTCAGAAAICAIGAIGTACAICCIICTICGICCICACCCTGT 514
                   338 TGGGCGACGCTTACTTCAGCGTCCCTCTGGACGA 371
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Sequence 11. Application US/10102622
Publication No. US203031931861.
GENERAL INFORMATION: AND P.
APPLICANT: Braun, Ralph P.
APPLICANT: Thomsen, Lindy
APPLICANT: Thomsen, Lindy
APPLICANT: War-Wally Catherine
APPLICANT: War-Wally Catherine
APPLICANT: War-Wally Catherine
APPLICANT: War-Wally Adjuvant
FITURE REFERENCE: 03367-021
CURBERT PATING DATE: 2002-03-19
CURBERT FILMS DATE: 2002-03-19
CURBERT FILMS DATE: 2002-03-19
CURBERT FILMS DATE: 2002-03-19
CURBERT FILMS DATE: 2002-03-19
CURBERT FILMS DATE: 2007-03-19
CURBERT FILMS DATE: 2007-03-19
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US-10-311-455-912/C
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est Local Similarity 46.5%; Pred. Mo. 0.032; 4.03
Matches 123; Conservative 0; Mismatches 144, Indels 0; Gaps
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Secre 38; DB 12; Length 1689;
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OTHER INFORMATION: nucleotide sequence of the coding insert in OTHER INFORMATION: $731-RT3
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GenCore version 5.1.6
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December 5, 2003, 14:16:11; Search time 1565.42 Seconds (without alignments) 9799:969 Million cell updates/sec 1 ccctcccttccgagctgagc......gaagccgccagcccagaag 375 OM nucleic - nucleic search, using sw model US-09-936-680-4_COPY_1_375 Title: Perfect score: Sequence: Run on:

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Searched:

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AX039100 1261 bp Sequence 4 from Patent W00063367. AX039100. GI:11229276	Hemo sapiens (human) Hemo sapiens Hemo sapiens Hemo sapiens Hemo Heazoa, Chordata; Craniata, Vertebrata, Euteleostomi, Hemalia; Eutheria, Primates; Catarrinii, Heminidae; Homo. Cox, P. Dixon, A. Jackson, A and Morgan, X. A novel family of beta sub-unit proteins from a voltage-gated sodi um channel, nucleic acids encoding them and therapeutic or
RESULT 1 AXO39100 LOCUS DEFINITION ACCESSION VERSION KRYWORDS	SOURCE ORGANISM REFERENCE AUTHORS TITLE

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AUTHORS Morgan.K. IIIIE Direct Submission OUNDAILS. Submitted (13-MAR-2000) Morgan K., Blochemistry, University of Cambridge. Termis Courts Road, Cambridge, CB2 10W, UNITED KINDOM COMMENT On Mar 14, 2000 this sequence version replaced gi:1160974. FEMUNES I1261 Corpations—Femula Submitter (1262) Author Court (1262) FEMULES (1262) Author Court (1262) Auth	gene 1.124 Type=Dzain 5.UTR (gene 2.03b" CDS (gene 2.03b) (gene 2.03b) (gene 2.03b) (gene 2.03b) (fene 2.03b) (fene 2.03b) (fene 2.03b)	Vordic sater Vord	Query Match 100.01; Score 375; DB 9; Length 1261;	AMACTICAMPTOCOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICAMPTICAMPTICAMPTICAMPTICACOCCONSTRUCTORY AMACTICAMPTICAMPTICAMPTICAMPTICATICAMPTICAMPTICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICATICAMPTICAMPTICATICAMPTICA
JOURNAL Dates: We see there of Journal Patent: WO 0053167-A 256-OCT-2000; RARNER-LAMBERT COMPANY (US) ; Cambridge University Technical Service Linited (GB); Cambridge University Technical Location/Qualifiers 1.1264 Companies	Ouery Match 100.08; Secre 375; DB 6; Length 1261; Best Local Similarity 100.08; Perel No. 9.88-70; Matches 375; Conservative 0; Mismatches 0; Indola 0; Gaps 0; Oy 1 CCCTCCTTCCGAGCTGAGCTTACCTCGAGCGCGAAACGAGCGGCGAAGGGCCCCAAACGAGCGCCAAGGGCCCAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCAAGGGCCAAGGGCCAAGGGCCAAGGGCCCCAAGGGCCCAAGGGCCCAAGGGCCCCAAGGGCCCCAAGGGCCCAAGGGCCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGCCCAAGGGCCCCAAGGGCCCAAGGGCCCAAGGGCCCCAAGGGCCCAAGGGCCCAAGGGCCCAAGGCCCAAGGCCCAAGGCCCCAAGGCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCAAGGCCCCAAGGCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCAAGGCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCAAGGCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCCAAGGCCCAAGGCCCAAGGCCCAAGGCCCCAAGGCCCAAGGCCCCAAGGCCAAGGCCAAGGCCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGGCCAAGCCAAGGCCA		241 241 301 301	OF 361 COCCAGCOCAGGARG 375 Db 361 COCCAGCOCAGGARG 375 BESULT 2 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 HARA2396 AZ3496 AZ34396 AZ3496 AZ34396

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303 AGANTCTGAGAGGGCGAGTCCTTGACCGAGGGATTCTCTCTGTGTAGCCTTGGAACCG 362
28822 AGANTCTGAGAGGGCGCAGTCTTTAACCGAGGAATCTCTCTGTGTAGCCTTGGAAGGCC 28773
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/chromosome="11"
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* runs of M. but the exact misses of the gaps are unknown.

* This record will be updated with the finished sequence 
* as soon as it is available and the accession number will 
* be preserved.
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       Homo sapiens (human)
Homo sapiens
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                                          ORGANISM
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50113 CCTICCTICGGTCAGAAAGTCGCCCCTGGGGGGCAGTTCGTCCTAAAGGGTTTCCTCGAA 50054
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                                                                                                       NOTE: Betimated insert size may differ from sequence length
(see http://www.hgac.bom.tmc.edu/doc/denbank_draft_data.html).
NOTE: This is a "working draft" sequence. It currently
consists of il contige. The true order of the pieces
is not known and their order in this sequence record is
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                                                 Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50293 GCTGGAGTTCCGGGGGGGGGGGGGGGCGACTGTCGTGGTGCTGAGGGCGGCGAGGC
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                   Estimated insert size: 139078; sum-of-contigs estimation
                                                                                                                                                                                                                                                               arbitrary, Gaps between the contige are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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    144833
/organism="Homo sapiens"

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/db_xref="taxon:9606"
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Best Local Similarity 100.0
Matches 373; Conservative
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Memmalia: Butheria; Permates; Catarthin; Hominidae; Homo.

11 (Dases) to 24423) Micho-Godola, B. Ali-Geman, R. A. Aliboro,
Alabrooks; J. Las Amaritumge; H. C., Are, J. R., Ayele, M. Banke, T.,
Barboris, J., Barke, S., Brider, M. Barborn, B., Blantehning, K. Bornin, D.,
Bouck, J., Caster, M., Cavazos, S. R., Chacko, J., Chavaz, D.,
Carron, T. F., Caster, M., Cavazos, S. R., Chacko, J., Chavaz, D.,
Carron, T. F., Caster, M., Cavazos, S. R., Chacko, J., Chavaz, D.,
Carron, T. F., Caster, M., Cavazos, S. R., Chacko, J., Chavaz, D.,
Carron, T. F., Caster, M., Cavazos, S. R., Chacko, J., Chavaz, D.,
Carron, T. F., Caster, M., Cavazos, S. R., Chacko, J., Chavaz, D.,
Carron, T. C., Gordon, C., Choyle, M. D., Danhere, S. R., Darda, R.,
Douthmatte, K. J., Deger, H., Deman, D., Markin, M. H.,
Douthmatte, K. J., Deger, H., Deman, P., Hale, S., Hamiton, K.,
Garbas, M., God, J., Gartin, M., Mangan, R., Charle, J., Borece, P., Frantz, P.,
Ralls, M., God, J., Gartin, M., Marke, M., Mall, M., Hale, S., Hamiton, K.,
Garbas, M., God, J., Gartin, M., Marke, M., Mall, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M., Marke, M.,
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Submitted (12-Mpt.)
Submitted (12-Mpt.)
Submitted (12-Mpt.)
Submitted (12-Mpt.)
Baylor Plaza, Housen, Tay 77030, USA
3 (Dases 1 to 144833)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: De-primer Bodlay: 144 of reads
Assembly program: Propy version 0.90029
Assembly program: Propy version 0.90029
Assembly program: Program: Program: Procomerus quality: 127266 bases at least Q40
Concessus quality: 127315 bases at least Q40
Concessus quality: 137315 bases at least Q40
Concessus quality: 13518 bases at least Q40
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Chemistry: Dye-primer E
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Unpublished
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* runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will be preserved.
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     ACUZ1981 149800 bp DNA linear HTG 19-JUL-2000 ROMS Bapiens Chromosome 11 clone RP11-11C15 map 11, WORKING DRAFT SEQUENCE, 29 unordered pieces.
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Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Sequencing vaccors, MII; W77875; 1004 of reads
Chemistry: Dye-terminator Big Dye; 1008 of reads
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-11C15
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ACO21981.2 GI:9280747
HTG; HTGS PHASE1; HTGS_DRAFT.
HOMO sapiens (human)
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**Overlap relationships among clones to be deduced.**

**Overlap relationships among clones to be deduced.**

**Ill be sequenced completion in the this clone will be sequenced in updated, the accession number will be
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Contact: sequence submissions@genome.wi.mit.edu
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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HOMO Sapiens clone RP11-20H9, LOW-PASS SEQUENCE SAMPLING.
AC013796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 122; DB 2; Length 66980;
Pred. No. 2.7e-16;
); Mismatches 0; Indels 1.
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Homo sapiens (human)
Homo sapiens
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Matches 133; Conserv
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Submitted (15-80v-1999) Whitehead Instruct MyT center for Genome Research J. 20 Charles Street, Cambridge, MA 02141, USA On Jan 27, 2001 Lithis sequence version replaced ii 7592586. All repeate were identified using Repeathwaker:
Smit, A. A. & Cenem, P. (1995-1997) http://ftb.genome.weshington.edu/WM/Repeathwaker:html Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Mu,X., Myan,D., Ye,W.J., Zimmer,A. and Zody,M.

Center: Whitehead Institute/ MIT Center for Genome Research Web site: http://www-seg.wi.mit.edu

expending reade that have not been assembled into contigs. The nation of N are used to separate the reads and the order in which they appear is completely and their order in which they appear is completely atheristry. Government among the second is deministry to closes that may be agent-rich and allower and the completely in the second close of the completely. The work is about not be assumed that this scione movement is module into be assumed that this scione where the completely in the event that the record is updated, the accession number will be appeared. NOTE: This record contains 83 individual

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us-09-936-680-4_copy_1_375.rge

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Best Local Similarity 51.0%; Pred. No. 0.27; Tidels 0; Gaps 0; Matches 122; Conservative 0; Mismarches 117; Indels 0; Gaps 0; As decocached and conservative 0; Mismarches 117; Indels 0; Gaps 0; As decocached and conservative 0; Mismarches 117; Indels 0; Gaps 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached and conservative 0; As decocached 0; As decocache	RESULT 14 STATA126 CARTAGO CART	* as soon as it is available and the accession number will * be precaved. * 52.14 52.13: contage of 532.19 bin length * 35.14 75.15: contage of 532.29 bin length * 45.16 74.75: contage of 100 bp * 74.76 87.77: contage of 100 bp * 75.76 74.75: contage of 100 bp * 75.76 74.75: contage of 100 bp * 75.76 74.75: contage of 100 bp * 75.77 100 bp

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tive 0; Mismatches 174; Indels 5; Gaps
1309 others
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All repeats were identified outsng RepeatMasker:
Smit, A. R. A. & Green, P. (1996-1997) Smit, A. R. A. & Green, P. (1996-1997) Http://ftb.genome.washington.edu/RW/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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                Wammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Sequencing vectors, mil; MTSPES; 1000 of reads
Sequencing vectors, mil; MTSPES; 1000 of reads
Assembly program Phrzap, vectation 0.96073 reads
Consensus quality; 123312 bases at least Q40
Consensus quality; 123387 bases at least Q40
Consensus quality; 142804 bases at least Q20
Insert size: 130000, agarcee.fp
Insert size: 130000, agarcee.fp
Quality coverage: 5.1 in Q20 bases; searce-fp
Quality coverage: 5.1 in Q20 bases; searce-fp
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                                                (bases 1 to 148643)
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65670 GCGGGCGCCTCCCACCTCGGCCTCCCAGTGTTGAAATTACAGGCGTGAGCCATGGCCCCC 65611 g

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306 ATCTGAGAGGCAGACCTTGACCGAGGGAATCTCTCTGTGT 348 g

Search completed: December 5, 2003, 20:51:01 Job time : 1572.17 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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December 5, 2003, 14:12:31; Search time 141.257 Seconds (without alignments) 7166.298 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

375 1 cottocottocgagotgago.....gaagoogocagoccagaag 375 US-09-936-680-4_COPY_1_375 Title: Perfect score:

Scoring table: Sequence:

2552756 segs, 1349719017 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched: 5105512

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a core greater than or equal to the sorse of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human beta3 CDWA. Human signal trans Human Ser-derived Human polypucioci Pull length human DWA encoding novel Bovine SET associa Human CDWA differe
£	AACG 9837 ABA93727 AAH9820 AAK5245 AAZ4053 AAZ4053 ABX837073 ABK837073
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* Query Match Length DB	100.0 98.6 4052 24, 76.9 978 22, 76.9 1048 22, 10.7 2806 20, 10.7 2811 23, 10.6 395 24,
Query Match	200.0 98.6 76.9 76.5 10.7 10.6
Score	369.8 288.4 286.8 40.2 40.2 39.8
Regult No.	

Cox P, Dixon A, Jackson A, Morgan K;

936 24 NBK73545 11727 24 NBK73545 11727 22 NBK73545 11727 22 NBK73515 11727 23 NBK73515 11727 24 NBK735	Bacillus lichenifo	Mouse ischaemic co		Human p21-activate	Human serine/threo	Novel human cDNA s	Human ORFX ORF2459	DNA encoding human	Chicken beta-actin	Chicken beta-actin	Expression vector	Hybrid promoter of	Chicken beta-actin	Mouse Meg1/Grb10 n	C-terminally trunc	Plasmid pCX nucleo	Rat expression pro	Plasmid pCX-eGFP n	Human expression p	Hprt gene containi	Mitochondrial beha	Positive selection	Plasmid pCXLamintR	Plasmid pCX-Lamint	Artificial plant c	Recombinase domain	Plasmid pl8attBZeo	Positive selection	pCAGGS-hSEPOR2 rat	Recombinase domain			Human pES31-alpha-				Plasmid plagenEPO
	ABK73545	ABI99475										-		AAH2179							-	-				ABT0819	ACC4472	ABK4952		-		ACC4471	AAD1273	ACC4472	-		Ċ
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                  (WARN ) WARNER LAMBERT CO. (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
                          AAC67837 standard; cDNA; 1261 BP.
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                                                                                                                                                                                                                                                                                                24-FEB-2000; 2000WO-EP01783.
                                                                            15-FBB-2001 (first entry)
                                                                                                     Human beta3 cDNA.
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                                                                                                                                                                                                                                                                                                                           15-APR-1999;
                                                                                                                                                                                                                      Homo sapiens.
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                                                 AAC67837;
RESULT 1
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Mon Dec

WO200198454-A2.

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123 GGGCGCGCAGCCGCTCATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAGGG 182
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                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA sequences and clones derived from human fetal brain, fetal
kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
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                                                                                                                                                                                                           (GEHU-) GERMAN HUMAN GENOME PROJECT.
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                                                                                                                                                           25-APR-2000; 2000US-199380P.
                                                                                                       25-APR-2001; 2001WO-IB02050
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                                                                                                                                                                                                                                                                                The present sequence is given in the claims of a specification will are several family of beta sub-mits procesise from a voltage of which there which have been collectively identified as beta, have been isolated the polymoclecture and antegonisers of social collectives and solypepticides are useful for screening for agonisers and antegonisers of social collections and mucleic social may be used diagnosting of treating diseases or conditions associated with voltage-gated socials contently and expension of the special solutions explains the paragraphic of the processing of treating diseases or conditions associated with voltage-gated socials concerning the paragraphic man, beneat disease. Society Systems of the paragraphic of the processing the paragraphic of the processing of treating diseases.
                                                                                          Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polygeptides, usefull for detecting and treating sodium channel-associated conditions, e.g. pain, lepsy and scroke
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100.0%; Pred. No. 5.7e-83;
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                                                                                                                                                                                                                                         Claim 10; Page 70-71; 88pp; English
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                         WPI; 2000-665241/64.
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550 610 242 670 302 790

122

AAKS2345 standard; cDNA; 1045 BP.

(first entry)

12-OCT-2001

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The invention relates to polymonicaties (AMX545-AMX5455) and the encoded polypeptides (AMX9323-AMX90302) that satisfie activity elazing optical projection of cell differentiation or which may induce production of other optokines in other cell populations. The polymonication of other optokines in other cell populations. The polymonication and polymonication are income or peptide and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities e.g. seem cell growth factor activity, hemanogodesis regulating activity induced production of the diagnosis and/or registering of many per useful in the diagnosis and/or registering or once; lenkamia, nervoka speem disorders, arithritis and
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                                                                                                                                                                                                                                                                                                                   Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; yeme cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; canoer; leukaemia; nervoue system disorder; arthritis; inflammation; es.
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Note: Records for SEQ ID NO 2110 (AAX52581), 2111 (AAX52582) and 3866
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Local Similarity 95.8; Score 286.8; DB 22; Length 1045;
Local Similarity 99.3; Pred. No. 2.7-6-61;
Les 288; Conservative 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                               Human polynucleotide SEQ ID NO 890.
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2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
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01-SEP-2000; 2000US-0654936,
12-SEP-2000; 2000US-0653561.
20-OCT-2000; 2000US-0693323.
30-NOV-2000; 2000US-0728422.
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                                                                                                                                                                    (first entry)
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                                                                                                                                                                    06-NOV-2001
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Zhao QA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the protein and coding sequence of novel proteins from a variety of organisms including human dog, cat, horse, cow, pig2 hamster, monkey, macque, yease, bacteris, fruit fly, ease, urchin and townson, These were delived from expressed sequence cage (BSTS) from the organism of increast. They can be used in disgnostics, from the organism of Americated from control or assess boodwareity and for nutritional purposes. The present sequence is a cDNA bookwareity and for nutritional purposes. The present sequence is a cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use -
                                                                                                                                               Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomatey, longs seat utchin; expressed sequence tag; EST; diaponetics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; mutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
A, Zhang J, Werhman T;
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                                                                           Human EST-derived coding sequence SEQ ID NO: 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1, Page 299-300; 1275pp; English.
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17-JUL-2000; 2000US-0617746.
03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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143 GCTCCCTCGAACTGGGGAGGTCCAGTGGGGTTAGGGCCCCAAAGCCCCCACCGGGCT 202
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renal failure, oxidative stress-related neurodegenerative disorders (e.g. amylotrophic lateral sciences), selfathoors disease and latify syndrome), cancer, catiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and measugal disorders. The proceins may also be useful for cell growth regulation (e.g. in wound healing), T cell scrivation, mitosis control, and as immunosuppressants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 ACCCTGGGCGCAAACGAGCGAGGCAGGGCGCGAGTGGAAACTGGGAGTTCCGGGGTGGG
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dignostics, forensics gene mapping, identification of mutations 
responsible for genetic disorders or other traits and to assess 
biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.7%; Score 40.2; DB 20; Length 2806;
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 2806 BP; 523 A; 957 C; 869 G; 457 T; 0 other;
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0; Mismatches 103;
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Matches 102; Conservative
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG19308.
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                                                                                                                                                                                                                                                                                       TGACCGAGGGAATCTCTGTGTAGCCTTGGAAGCCGCCAGCCCCAGAAG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 365; 387pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ40538 standard; DNA; 2806 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressant; ss
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New nucleic acid associated with lactation, and musele and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle
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tches 86; Conservative
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standale deposition; for deposition; genome mapping; gene identification;
gene analysis; cattle breading.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 ACCCTGGGCGCAAACGAGGGAGGCAGGGCGCGAGTGGAAGCTGGAGTTCCGGGGTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40.2; DB 23; Length 2811; Pred. No. 1.3; 0; Mismatches 103; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2811 BP; 524 A; 957 C; 870 G; 460 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 10.7%;
al Similarity 49.8%;
102; Conservative (
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(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAO N.
WARREN W C.
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(WARR/)
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                                                                                                The invention relates to a purified nucleic acid molecule associated with
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0; Mismatches
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Claim 2; SEQ ID No 2238; 245pp; English
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157 gggaggrecagregorregetaggecenaagececeaececeg-crecaaaagetecea 215
                                                                                                                                                                                                                                                   ABK73545 standard; DNA; 936 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOVO ) NOVOZYMES BIOTECH INC.
(NOVO ) NOVOZYMES AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-0CT-2000; 2000US-0680598.
27-MAR-2001; 2001US-279526P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-OCT-2001; 2001WO-US31437.
                                                                                                                                                                                                                                                                                                                  13-AUG-2002 (first entry)
                                                                                                                                                                     2223 CTGGTCACCC 2232
                                                                                                                                       276 CAGTICGICC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sacillus licheniformis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berka R, Clausen IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-416684/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequenced tag array
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-2002.
                                                                                                                                                                                                                                                                                    ABK73545;
                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                   셤
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                                                                                                                                                                                                                                                                                                                                                       The invention relates to detecting (MI) granulocyte (GC) activation (GC). By detecting the level of expression of genes is (is) identified by GCC (GCA), by detecting the level of expression of genes is (is) identified by GCC the Appearance of GCA and and a series of the leaf one indication of GCA and a leves the series of GCA and a leves the series of GCA and a leves the series of GCA and a leves the series of GCA and a leves the series of GCA and a leves the series of GCA and a leves the series of GCA or an inflammation (especially character) in a tissue, an allergic response in a subject, exposure of a bubject to a pathogen or sterile inflammatory disease by detecting the chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a tissue, and allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the chronic) in a lingual sease. The sease of the sease of gene is the season of sease of the season of gene is the season of sease of the season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of gene is the season of season of gene is the season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of gene is the season of season of season of season of gene is the season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of season of sea
                                                                                                                                                                                                                                                Detecting granulocyte activation by detecting differential expression
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                                                                                                                                                                                                                                                                     of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24; Length 2685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the printed specification, but was obtained in electronic mat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.9;
0; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2685 BP; 495 A; 774 C; 966 G; 450 T; 0 other;
                                                                                                                                                                                         Vockley J;
                                                                                                                                                                                         Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39.6;
                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID No 313; 114pp; English.
                                                                                                                                                                                       Weissman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 50.0%;
Matches 125; Conservative
                                                                                            03-OCT-2001; 2001WO-US30821.
                                                                                                                          03-OCT-2000; 2000US-237189P.
                                                                                                                                                         (GENE-) GENE LOGIC INC.
                                                                                                                                                                                                                       WPI; 2002-435328/46.
                                                                                                                                                                                         Beazer-Barclay Y,
                                WO200228999-A2.
                                                                                                                                                                                                                                                                                                        drug toxicity
                                                              11-APR-2002
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97 CGGTGGTGCTGAGCGCCGGCGAGAGCGGCGCGGAGCGGCTGATCGGCTCCTCGAACTG 156

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216 GGGCTCCCCAGGCACCGGTGCTCGCCCTTCCTTCGGTCAGAAAGTCGCCCCTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Differential gene expression; genomic sequenced tag; GST;
altered oulture condition; environmental stress;
physiological provocation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus licheniformis genomic sequence tag (GST) #836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; SEQ ID NO 836; 200pp; English.
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174

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57 GTGGAAGCTGGAGTTCCGGGGTGGCGGAGGCGACTGTCCGTGGTGCTGAGCGCCGGC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 GAGAGCGGCGCGCAGCCGCTGATCGGCTCCTCGAACTGGGGAGGTCCAGTGGGGTCGC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 GAAGGGGGGGGGGGGGGGGGGGGGGGAGGAGCGAAAAGGCTTTTCCGCCCGGGAGC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a library of human polynucleotides comprising the sequences given in AMSI352 to AMSI7779, Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 TRAGGGCCCRAAGCCCCCCCCCCCCCAAAAGCTCCCAGGGCTCCCCAGGCACCGGTG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 Grégecreridece accedent contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de contrata de co
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; gene, gene expression product; diagnosis, therapy; probe; detection; mapping; tissue ryping; profiling; foremic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                   ö
      which are used in the exemplification of the present invention
                                                                                                                                                         10.4%; Score 39; DB 24; Length 3272; 48.4%; Pred. No. 2.7; tive 0; Mismatches 115; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gene expression product cDNA sequence SEQ ID NO:4735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Innis MA;
bat I;
Reinhard C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 CTCGGCCCTTCCTTCGGTCAGAAGTCGCCCCCTGGGGCAGT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 chiccogcicinitricing agenciación con consecuencia 337
                                                                                         Sequence 3272 BP; 878 A; 919 C; 752 G; 720 T; 3 other;
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AAZ17263 standard; cDNA; 1337 BP
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98US-0075954.
98US-0080114.
98US-0080515.
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                                                                                                                                                                                                      Sest Local Similarity 48.4
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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24-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ17263;
                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 CGTGCTGCTGAGCGCCGGGCGAGAGCGGCGCGGAGCGGCTGATCGGCTCCCTCGAACTGG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 GAGCGAGGCAGGGGGGGGGAGTGGAAGCTGGAGTTCCGGGGTGGGCGGGGAGGCGACTGTC 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for examining ischemic conditions, comprising measuring the expression profile of a geneal (1998). Set of the conditions of the conditions of the conditions are conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the condition of the c
specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse ischaemic condition related cDNA sequence SEO ID NO:431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
                                                                                                                                                                                                                                            10.4%; Score 39; DB 24; Length 936;
                                                                                                                                                                                                                                                                                                                               0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ishii Y;
                                                                                                                                                               Sequence 936 BP; 220 A; 190 C; 470 G; 55 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                   Pred. No. 2.3;
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                                                                                   ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABI99475 standard; cDNA; 3272 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAGGTCCAGTGGGG 172
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                                                                                                                                                                                                                                                                                         55.6%;
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                                                                                                                                                                                                                                                                                         Local Similarity 55.6
nes 75; Conservative
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the stage that of baing cancerous, where he gene product is encoded by one of the stage polynuclectide sequences given in AA21233 to AA21779. The polynuclectide are be used as a source of primars and probes, which can be used as a source of primars and probes, which can be used as a variety of purpose, e.g. detection of expression levels. Capaping, tissue typhing or profilling, forentiate, spentic analysis and detection of polynorphisms. Polypeptides encoded by the polynuclectides of the polynuclectide encoded by the polynuclectides may also be used to construct a rarys for diagnostic (which may be used to determine function of an encoded protectin); and to detect differences in expression levels between two colls (e.g. to identify a bonomal or diseased takens in a whome, to diseated the prognosts and management or susceptibility to a disease such as connect. The polynuclectides of the invention are especially the disease such as the disease such as the disease such as the disease and antagement of the polynuclectides can also be used to screen for expression and authosomises.
differentially expressed gene product in a test sample from a cell
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Seguence 1337 BP; 42 A; 577 C; 27 G; 22 T; 669 other;

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                                                                                                                                                               Gaps
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10.3%; Score 38.6; DB 20; Length 1337;
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                                                                                                                                                  Indels
                                                                  Pred. No. 3;
0; Mismatches 100;
                                                                  Local Similarity 41.5%;
nes 71; Conservative
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Query Match
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Human p21-activated kinase 4 (PAK4) DNA coding sequence. AAD06422 standard; DNA; 1776 BP. (first entry) 10-AUG-2001 AAD06422; RESULT 13

Human; p21-activated Kinase 4; PAK4; genetic mapping; neuroprotective; immunosuppressive; gene thetarpy; cancer; andiogenesis-related disorder; sering-thronine kinase; restriction fragment length polymorphism; RELP, central nervous system disorder; immune-related disorder; cytosteatic; da.

Homo sapiens

WO200136602-A2. 25-MAY-2001. 14-NOV-2000; 2000WO-EP10736.

(PHAA) PHARMACIA & UPJOHN SPA. 99US-0439756. 15-NOV-1999;

Galvani A; Moll J, WPI; 2001-355626/37. Dahlberg M,

New nucleic acid encoding p21-activated kinase 5 protein for inducing an immune response, trasting cancers, angiogenesis-related disorders Alsorders of the central nervous system and immune-related disorders

Example 1; Page 36-37; 76pp; English.

The present DNA sequence is the coding sequence (TDS) of human Dpl.

cuttated kinnes of (EAM4) DNA. The protein encoded by DAMI DNA is 687

identical to PASS protein which is a scrint-threonine kinnes. PASS is

cueful for inducing an immune response in a mammal against PASS is

cueful for inducing an immune response in a mammal against PASS is

cueful for inducing an immune response in a mammal against PASS is

polypeptide. PASS proteins are useful in replating of call profile cation,

cat migration, cell office progression, and cell death. PASS, is useful in

cut search Knowl against that can madify and/or control the above

controlled to the progression, and cell death. PASS, is useful in

controlled to the progression, and cell death. PASS, is useful as forth

controlled to the progression, and cell death. PASS, is useful as forth

controlled to the progression, and composite tools for probing

controlled to the progression of the controlled to the responses. PAKS DNA is also useful in gene therapy.

Sequence 1776 BP; 337 A; 616 C; 568 G; 255 T; 0 other;

367 hóchaceacchanaeacachanaeanhachachachachachachachachachanaea 426 23 ACCCTGGGCGCAAACGAGCGAGGCAGGCGCGCGCGTGGAAGCTGGAGTTCCGGGGTGGGC Gaps .. ; DB 22; Length 1776; 3.1; 0; Mismatches 104; Indels Score 38.6; Pred, No. 3. 10.3%; Matches 101; Conservative Query Match Best Local Similarity

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AAZ40657 standard; DNA; 1941 BP. RESULT 13 AAZ40657

Human serine/threonine kinase, PAK4 encoding DNA. (first entry) 08-MAR-2000 AAZ40657;

PAK4; serine/threonine kinase; GTPase; intracellular signal cascade; serio Cdc43H; morbogenesis mitogenesis; UNK p38 Mak kinase; human; acta polymerization; filopodia; cancer; arthritis; se.

Homo sapiens

WO9963073-A1.

09-DEC-1999.

99WO-US11341 21-MAY-1999;

UYCO) UNIV COLUMBIA NEW YORK. 98US-0082737. 21-MAY-1998;

WPI; 2000-072881/06. P-PSDB; AAY59128. Minden A;

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Ren

Zhao QA, Re Drmanac RT;

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The first invention relates to the comes encoding an isolated novel human polypeptide where the protein encoded but the much science of the protein encoded but the much card of the protein encoded but the much card of the control of the protein encoded but the much card of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87 AGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGCGGGCGCGGGGGCGCTGATCGGCTC 146
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                                                                                                                                                                                                                                                                                                                                                                  Novel polypoptide useful for treating neurodegenerative diseases and uppoid or lymphoid cell disorders, bone disorders, mentanital and traument disorders, and inflammatory diseases traument disorders, and inflammatory diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 TGGGCGCAAACGAGCGAGGCAAGGGCGCGCAAGTGGAAGCTGGAGTTCCGGGGGTGGGCCGGGG
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                                                                                                                                                                                                                     Zhang J,
Wang D,
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Pred. No. 3.
                                                                                                                                                                                                                 Liu C, Zhou P, Asundi V,
Yang Y, Wehrman T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page -; 612pp; English.
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29-JAN-2002; 2002WO-US01222
                                                               30-JAN-2001; 2001US-0774528
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                                                                                                                    (HYSE-) HYSEQ INC.
(GOOD/) GOODRICH R W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                     Tang TY,
Xue AJ,
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                                                                                                                                                                          The invention relaces to an isolated manualian ancides each that encodes by a novel cerime/brecomine tinage or its mutant bounding. Pake is an effector for the offresses has and cdecizis which are involved in the creatibute signal osciedes, morphogenesis and mitogenesis, and mitogenesis, and activates the JMK and page with the three series of this pathways. Inhibiting interaction of pake at the the three countries of the protein of the protein. In inhibiting the critin polymerization and formation of fliopodia. The PAKe with the type of the protein, and as a source of probes for identifying longologies gequences and of fallipense oilgomicated teles for identifying longology agenerices and of antil sense oilgomicated teles for identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibiting PAK4 expression. The protein, or its fragments are used to raise specific artibotics and these are useful as ligands for therspeutic inhibition of interaction between PAK4 and its marive binding partners. Inhibition of PAK4 activity or expression is used for treatment of cancer and artificial. The present sequence represents the DNA encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 ACCACGGCCAGAGGGGGCCCAGGGAAGGCAGGCAGGCCGAGGCCGGTTCGCCGGTCACAGC 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GGGGAGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGCGGGCGCGGAGCGGCTGATCG 142
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                             Novel mammalian nucleic acid useful for treating cancer and arthritis
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                                                                                                                    Claim 16; Fig 1A-B; 95pp; English.
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ID ABX70915 standard; cDNA; 2310 BP.
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Claim 5; Page 4092-4093; 5507pp; English.

AC74446 to AAC77666 encode the proteins given in AAB40237 to AAB43397, AAC74446 to AAC77666 encode the proteins given in AAB40237 to AAB43397, AAC74446 to human observation that have activities much as cyclectaid hepatotropid, vulnerary, occupants where activities much as cyclectaid; hepatotropid, vulnerary, occupants and activities much mannerary in the AAB40237 to Caractical and the AAB4023 to Caractical AAB40237 to Car coagulation, to inhibit thrombosis; and as a contraceptive Sequence 1544 BP; 209 A; 565 C; 499 G; 271 T; 0 other;

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1 Chases 1 to 100 Primates; Catartini, Hominidae; Homo.

1 Chases 1 to 100 Primates; Catartini, Hominidae; Homo.

1 Chases 1 to 100 Primates; Catartini, Hominidae; Homo.

Phil-Laght Chart.

Phil-Laght Chart.

Phil-Laght Chart.
Man Sequencine by, Agencourt Bioscience Corporation Conduction Clone distribution; MGC clone distribution; MGC clone distribution; information can be theup://image.llnl.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.com/mgC.gov.c
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19.19 1906 ENTX cedex - France
Emali: seqretégenoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 GGCCCTTCCTT--CGGTCAGAAAGTCGCCCCTGGGGGGCAGTTCGTCCC 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            519 GCTGGAGTTCCGGGGTGGGCGGAGGCGACTGTCCGTGGTGCTGTGGCGCCGGCGAGAGC
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http://fulllength.invitrogen.com/ InVirroden Corporation 1600
Faraday Avenue Genescope sequence ID : CS0DF005BE01QF1.
Locarion/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 346; DB 9;
Pred. No. 1.3e-69;
0; Mismatches 1;
                                                                                                                                                                                                organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                          /clone="CS0DF005YI02"
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Best Local Similarity 98.9°
Matches 369; Conservative
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BP 191 9106 EVRY cedex - FRANCE (F-mail : segrefégenoscope.cns.fr
Neb : www.gentocope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AAGCTGGAGTTCCGGGGGGGGGGGGGGGGGGGTGTGCTGGTGCTGAGGCGCCGGCGAGA 120
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BACROSH10 of RPCI-98 library from brosophila melanogaster (fruit
fly), genomic survey sequence.
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Neopeta, Endoperygota, Dipeta, Esachycera, Muscomorpha,
Sphydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
Mol type="genomic DNA"
/db xref="taxon:727"
/clone="pacR14N09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15.7%; Score 52, ____31.6%; Pred, No. 0.0012; five 85; Mismatches 145;
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/note="end : T7"
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            Invitrogen. Contact : Feng Liang Email : fliangelifetech.com Uhttp://fulllength.invitrogen.com/ Invitroden Corporation 1600 Faraday Avenue Genascope sequence ID : CLOBA0072H127P1. Location/Qualifiers
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Drosophila melanogaster
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/clone="CSODE005X119"
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Wir. The library is named RPCI-98 and was constructed by partial moost desertion of Drosophila DNb provided by the Bops from the acception circain y2; on he sp, the same strain used for the Bops Pr and RST libraries. A more detailed description of the library and how to order individual BMC clones, the entire library, or filters for hybridation from the BMCPR Resource Center on be found at http://bappe.med.
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/clone lib=Thom sapiens PLACERTA'.
/clone lib=Thom sapiens PLACERTA'.
/note="Netcor: pANNSPORT 6; lst errand cDNA was primed
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ogi-bni/dauser.cgi/seq-cSpAs0052000pt.gcluster=s789.f. Contact
Reng Liang Bmall. filangelistetech.com/ URL :
Frang Liang Bmall. invitrogen.com/ URL :
Fraday Nemus Genocope sequence ID : CSOAS00520020pt.
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On Feb. 13. 7001 this sequence version replaced gi:12802039.

On Feb. 13. 7001 this sequence version replaced gi:12802039.

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Matches 131; Conservative
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Pan troglodytes DNA, clone: PTB-047116.F, genomic survey sequence.
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Toyocki,Y., Matanabe,H. and Sakaki,Y.
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/mol_type="genomic DNA"
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57
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Mammalia, Buthoria, Primates, Catarrhini, Hominidas, Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:7227"
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12.5%; Pred. No. 0.11;
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/note="end : TET3"
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KEYWORDS
SOURCE
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AUTHORS
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GenCore version 5.1.6
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nucleic search, using sw model OM nucleic

5, 2003, 17:21:16 ; Search time 33.0095 Seconds (without alignments) 5014.271 Million cell updates/sec December Run on:

1 ccctcccttccgagctgagc.....gaagccgccagccagaag 375 US-09-936-680-4_COPY_1_375 375 Title: Perfect score: Sequence:

569978 segs, 220691566 residues Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table: Searched:

1139956 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the cocla score distribution.

SUMMARIES

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Result		Query				
No.	Score	Match	ra.	DB	ID	Description
-	44.8	11.9	11558	2	PCT-11593-06251-23	Land CC democracy
N	38.6	10.3	1941	n	US-09-082-737-1	Semience 23, Appl
3	37.2	6.6	152331	m	US-09-128-155-16	1 2
0	36.2	9.7	2608	4	US-09-904-615-16	16
0	36.2	9.7	38506	m	US-09-320-878-19	10
9	36.2	6.6	38506	4	US-09-141-908-1	1
c 7	36.2	9.7	38506	4	US-09-657-440-19	Sequence 19. Appl
80	36	9.6	1020	4	US-09-252-991A-198	100
٥ ٥	35.8	9.5	1342	m	US-08-445-515-52	2
0 70	35.8	9.5	1342	m	US-08-445-515-53	2
11	35.8	9.5	3521	4	US-09-484-970B-104	0
c 15	35.6	9.5	6152	н	US-08-557-139-1	-
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0 14	35.4	9.4	1994	s	PCT-US94-10261A-22	2
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c 16	35.2	9.4	5496	e	US-08-600-982-23	2
c 17	35.2	9.4	5496	ഗ	PCT-US94-10261A-23	3
18	35.2	9.4	16595	4	US-09-146-053-7	
c 13	34.8	9.3	834	4	US-09-252-991A-740	74
20	34.8	9.3	1104	4	US-09-252-991A-645	645
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c 24	34.6	9.5	1269	4	US-09-252-991A-3470	
c 52	34.6	9.5	1969	m	US-09-098-628-1	1 An
c 26	34.6	9.5	13842	m	US-09-105-537-30	2
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		426	4	US-09-397-787-212	212	_
4 3 3 3 3 3 4 6 9 9 7 6 9 4	9.1	2271	4	US-09-052-521C-3	Sequence 3, Appli	
20000000000000000000000000000000000000		936	4	US-09-252-991A-14414	7	_
37 38 39 40	9.1	1494	4	US-09-252-991A-14285		_
7 8 8 6 4 4 9 8 8 4		2239	4	US-09-581-831-1	Sequence 1. Appli	
388		4600	4	US-09-702-705-1797	-	
39	9.0	4600	4	US-09-736-457-1797		_
40		7218	٦	US-08-232-463-14	Sequence 14. Appl	
		12847	н	US-08-550-715-1	Sequence 1. Appli	
41 33.6		564	4	US-09-252-991A-11689	7	
42 33.6		1080	4	US-09-252-991A-11765	_	_
43 33.4		43280	8	US-08-804-227C-1	-	
2 44 33.2	8.9	588	4	US-09-252-991A-5858	Sequence 5858. Ap	_
45	8.9	1335	s	PCT-US91-06532-1		

ALIGNMENTS

Sequence 21 Fablication Pc/TUS9306251

ADPREAL INFORMATION: DATA and Sife, Jason P.

ADPREAL INFORMATION: Trivalent Synthesis of Oligonucleotides Containing TITE OF INVERTION: Extraolent Synthesis of Oligonucleotides Containing TITE OF INVERTION: Stateospecific Alkylphosphonates and Arylphosphonates CONTAINES: ADPRESSES: SCULLY, SCOTT, MARRHY & PRESSER

STREET: 400 GAZden City Plaza

CITY: GAZden City Plaza CT-US93-06251-23 RESULT 1

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ATYONEY/AGENT INFORMATION:
NAME: DIGIGGIA, FRANK S.
REGISTRATION NUMBER: 31,346
REFERENCY/DOCKET WINBER: 6866
TELECOMMUNICATION INFORMATION:
TELECHONE: 516,142,434

TELERA: 116-772-4366
TELEX: 230 901 SANS UR
TELEX: 230 901 SANS UR
SEQUENCE CHRACKELS: 1CS:
LENGTH: 11558 Dase pairs
TYPS: mclaic acid
STRANDEDWSS: double MOLECULE TYPE: DNA (genomic) linear PCT-US93-06251-23 TOPOLOGY:

Gaps 7; Length 11558; Indels Score 44.8; DB 5; Pred. No. 0.015; 0; Mismatches 77; Query Match Best Local Similarity 56.7%; Matches 102; Conservative

133 74 GGGGTGGGCGGGAGGCGACTGTCCGTGGTGCTGAGCGCCGAGAGCGGCGAGAGC

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134 GGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCG-CTTAGGGCCCAAAGCCC 192

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                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT FAIL YES AND THE APPLICANT FAIL OF THE APPLICANT FAIL YES APPLICANT SHOULD SO F TANGO-77 RELATED PROTEIN FANILY TITLE OF INFORMATION: NOVE MOLECULES OF TANGO-77 RELATED PROTEIN FAIL OF APPLICATION NUMBER: US /09/128,155 CHERENT FAILNE APPLICATION NUMBER: US /09/1650 CHERENT FAILNE APPLICATION NUMBER: US /09/1650 CHERENT FAIL OF APPLICATION NUMBER: US /09/1650 CHERENT FAIL OF APPLICATION NUMBER: US /09/1650 CHERENT SAPLICATION NUMBER: US /09/1650 CHERENT FAIL OF APPLICATION N
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1. Similarity 9.7%; Score 36.2; DB 4; Length 2608;
1. Similarity 94.0%; Pred; No.1.8;
1.4; Conservative 0; Mismatches 63; Indels 0
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Sequence 16, Application US/09904615
Sequence 16, Application US/09904615
September 1711000 US/09904015
TITME REPREMENT PEAGLAP PROGRET US/09/904,615
CURRENT APPLICATION WURBER: US/09/904,615
CURRENT PILION DATE: 1200-00-13
PRIOR APPLICATION WURBER: 05/09/91
PRIOR APPLICATION WURBER: 66/09/91
PRIOR APPLICATION WURBER: 66/09/91
PRIOR APPLICATION WURBER: 66/09/91
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                                             US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: (1)...(152331)
OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 74; Conserva
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488 TGCGGAGCGGGGCTCGACGCGGGGCGCTGGCGGCGGAGTGTATGCAGACGCGC 547
                                                                                                                                                 532 ÁCCACGGCCAGAGGGGCCCAGGGAAGGCAGCCAGCCGAGGCCGGTTCGCCGGTCACAGC 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652 TCCAGGGAGGCTCAGGGGGTCCCCAGGAGTCCTCCCGGGACAACGCCCCCCTCTCCGGG 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09082737

Reserve No. 6013500

RENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TORRESPORTER DESIGNES:
CORRESPORTER DESIGNES:
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CURRENT APPLICATION NUMBER: US/09/082,737
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
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TELEPAX: (212) 391-0525
INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS:
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ZIP: 11230
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APPLICANT: SHELKA, GALY
APPLICANT: SHELKA, GALY
APPLICANT: BETLACH, Welanie C.
APPLICANT: WINDANIEL, Robert
APPLICANT: WINDANIEL, Robert
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CRGANISM: Streptomyces venezuelae
US-09-141-908-1
Sequence 1, Application US/09141908
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Patent No. 6117659
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; ORGANISM: Streptomyces venezuelae
US-09-320-878-19
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APPLICANT ASHLEY GATY
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MORNIEL, Robert
APPLICANT: TANGA, Li
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LENGTH: 38506
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                                                                                                                                                                                                                    Sequence 52, Appl.cation US/08445515
Patent No. 644308
GRNEAL INFORMATION:
APPLICANT: Beaces Milliam B.
TITLE OF INVERTION: A No. 66430884 Prostate/Colon Tumor Suppressor
TITLE OF INVERTION: A No. 66430884 Prostate/Colon Tumor Suppressor
MINMER OF SEQUENCES: 59
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APPLICANT: Bascs, Milliam B.
APPLICANT: Sancs Milliam B.
APPLICANT: A No. 6041089al Prostate/Colon Tumor Suppressor IIILE OF INVENTION: Gene Located on Human Chromosome 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell and Flores
STREET: 4370 La Jolia Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEDDIN TYPE: POppy disk
CMMPUTSR: THW PC Compatible
CMMPUTSR: THW PC Compatible
SPRATTNG STSTEM: PC-2006/M9-LOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPL/CATION NUMBER: US/00/445,515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-CJ 1607
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Patent No. 6043088
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPRA; (619) 535-8949
INFORMATION FOR SEQ ID NO: 52.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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CLASSIFICATION: 435
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CITY: San Diego
STATE: California
COUNTRY: USA
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US-08-445-515-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                       US-08-445-515-52/c
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APPLICANT: MACO 1 Rubenfield et al.
TITLE OF INVENTION: MUCLIC ACID DAND ANIDO ACID SEQUENCES RELATING TO PESUDOMONAS
TITLE OF INVENTION: MUCLIC ACID DAND ANIDO ACID SEQUENCES RELATING
TITLE OF INVENTION: MUCLIC ACID DAND ANIDO ACID SEQUENCES
CORRENT APPLICACION NUMBER: 1059/10218
PRIOR PLIAND DANE: 1999-102-18
PRIOR APPLICACION NUMBER: 05 60/094,130
PRIOR APPLICACION NUMBER: 05 60/094,130
NUMBER OF SEQ ID NOS: 33142
LENGHER 1039
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9.7%; Score 36.2; DB 4; Length 38506;
Bost Local Similarity 45.6%; Pred. No. 2.5;
Natches 128; Conservative 0; Mismatches 153; Indels 0;
Natches 128; Conservative 0; Mismatches 153; Indels 0;
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Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                TYPE: DNA
CRGANISM: Streptomyces venezuelae
US-09-657-440-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 19
LENGTH: 38506
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US-09-252-991A-198
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1312 TGGCGGTGGCAATAGGCCCAAGGCTGGGACCCAAGCTGAAAGCCTGTAGGAGTGGGCCCAAG 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AGCGCCGGCGAGAGCGGGCGCGGGGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 TGGGGTCGCTTAGGGCCCCAAAGCCCCCACCGGCTCCAAAAGCTCCCAGGGCCTCCCCAG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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STREET: 405 Lexington Avenue
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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.1%; Pred, No. 2.3;
Bast Local Similarity 53.1%; Pred, No. 2.3;
To, Conservative 0; Mismatches 67; Indels 0
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Best Local Similarity 51.2%; Pred. No. 2.8;
Marches 83; Conservative 0; Mismatches 79; Indels 0.
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APPLICANT: Pedersen, Oluf
APPLICANT: Pedeersen, Karbrine A.
APLICANT: Picture Christian A.
APLICANT: Picture MUTANT DNA BNCODING INSULIN RECEPTOR
TITLE OF INVENTION: SUBSTRATE 1
CORRESPONDENCE A.DORESS:
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OTHER INFORMATION: Incyte ID No. 6426186 407143.2CB1
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; Patent No. 5827730
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FEATURE:
                                                      NAME/KEY: unsure
LCCATTON: 3139
CTHER INFORMATION: a, t, C,
US-09-484-970B-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELERAX: (212) 8/8-9655
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 6152 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581..4309
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STATE: New York
COUNTRY: USA
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US-08-557-139-1/c
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; LOCATION:
US-08-557-139-1
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9.5%; Score 35.8; DB 3; Length 1342;
Best Local Similarity 47.5%; Pred No.2,
Best Local Similarity 67.5%; Pred No.2,
Best Local Similarity 67.8%; Pred No.2,
Best Local Similarity 67.8%; Danatches 112; Indels 67.8%; Danatches 112; Danatches 67.8%; Danatches 112; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Danatches 67.8%; Dan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDZIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COMPATING 1927EM: PC-DOS/MS-DOS
SOFTWARE: PREDERTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                            E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 GCTCCAAAAGCTCCCAGGGCCTCCCCAGGCACCGG 234
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Retent No. 642456
Retent No. 642456
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ATTORIST/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION WINBER: 31 815
REFERENCE/DOCKET NUMBER: 9-CJ 1607
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/445,515
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-894
INFORMATION FOR SEQ ID NO: 53-8849
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
NUMBER OF SEQUENCES: 59
                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ORCANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                            92122
                                                                                                   ADDRESSEE:
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658 TCATCACACAGGIGICGCAATCATCATCTTCTGCAGGGTTGTTATCTTTG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 TTTCCTCGAAAGAATCTGAGAGGCGCAGTCCTTGACCGAGGGAATCTCTCTG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 rearcacacaderorcecaarcarcarricarienecadoserrenariaria 606
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DESCRIPTION: CDNA sequence corresponding to FIGURES 11A-11C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.4; DB 5; Length 1994; Pred. No. 2.7; 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Christensen, O'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
CITY: Seattle
                                                                                                                            TUTS94-10cath-21c/C
Sequence 22, Application PC/TUS9410261A
GREERAL INFORMATION:
APPLICANT: Cartez, Milliam G.
APPLICANT: Gl., Semanna A.
APPLICANT: Gl., Semanna A.
APPLICANT: Ryan, Maureen C.
TITLE OF INTENTION: Epiligrin, an Epithelial Ligand for TITLE OF INTENTION: Integrins
WOMBER OF SECURIORS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10261A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA

ZIF: 9810.128.00

ZIF: 9810.128.00

ZIF: PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Shelton, Demnis K.
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOM (682-8100
TELEFRX: (266) 224-0779
INFORMATION FOR SEQ. ID NO: 22:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09679279
Patent No. 6524841
GENERAL INFORMATION:
APPLICANT: MCDAniel, Robert
APPLICANT: Volchegursky, Yanina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 50.3%;
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1994 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: HOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US94-10261A-22
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US-09-679-279-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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                                             431 CGGGGAGGGGCAGCTGAAGGAGGACGCAGCTGCTGAGCCCCAGGAGAGGCCCGACCGGAG 372
                                                                                                                                                         371 TTTTCGGGCGCTTCACGCCCGGCGGGAAGCCAGTGCGTCCGGGGTGAGGGCAGCCCCGAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 TGGCTTAGGGCCCAAAGCCCCCCACCGGGCTCCAAAAGCTCCCAGGGCCTCCCCAGGGCACC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    778 TGGCCTGGGTCTCCATGTGCCTCATCTGCTCCAGAAGCCCTGCGCTGGCACTCAGGCCT 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 GOTGCTCGGCCCTTCCTTCGGTCAGAAAGTCGCCCCCTGGGGGCAGTTCGTCCCAAAGGG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659
                                                                                                       133 CGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAGGGCCCCAAAGCCC 192
    718 GCAGCTGAGACTTGACCAGGCGGAGCTGCTCGCCCATGGTGGCCAGGTCGTTCAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 ITTCCTCGAAAGAATCTGAGAGGGCGCAGTCCTTGACCGAGGGAATCTCTCTG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.4; DB 3; Length 1994; Pred. No. 2.7; 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Christensen, C'Connor, Johnson, and Kindness
STREET: 1420 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Catter, william G. APPLICANT: Catter, william G. APPLICANT: Cil. Susanna A. APLICANT: Nyan, Waureen C. TITLE OF UNWERTON: Epilágin, an Epithelial Ligand for TITLE OF UNRESTON: Integrins
                                                                                                                                                                                                               193 CCACCCGGCTCCAAAAGCTCCCAGGGCCTCCCCAGGCACCGG 234
                                                                                                                                                                                                                                                             31.1 cércégadadéchagererecrérendécedécedechechage 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA to mRNA CDNA sequence corresponding to FIGURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/600,982
FILING DATE: 02-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 98101-8100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    US-08-600-982-22/c
; Sequence 22, Application US/08600982
Ratent No. 6120991
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY, JARRY TREABMATON;
NAME: Shalton, hennia X.,
REGISTATION NUBERE: 26, 997
TELECOMONICATION INFORMATION;
TELEFOR: (206) 682-8100
INFORMATION (206) 224-0779
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.3%;
Matches 87; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: N
ORIGINAL SOURCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION:
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Modelson: (19566)...(43271)
OFFICE TO THE MANAGEMENT OF MEGALITY, SEQ ID NO: 15= translated amino acid sequence
MANAGEMENT (19766)...(19576)
MANAGEMENT (19766)...(19576)
MANAGEMENT (19766)...(19576)...(19769)
OFFICE INFORMATION: megalil, ATS
MANAGEMENT (19766)...(19769)
OFFICE INFORMATION: megalil, ATS
MANAGEMENT (19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(19769)...(
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ACCATION: (26230)...(26733)
THER INFORMATION: megAlI, KR3 (inactive)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURE/NEW TREE SERVED STATE OF THE MURE/NEW TREE SERVED STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF THE MUSE STATE OF TH
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COCATION: (17155)...(1764)
OTHER RIPORANTOR: megAl. RR1
MANG/KET ming cleature
COCATION: (1737)...(1827).
COCATION: (1737)...(1827).
COCATION: megAl. ACP1
COCATION: ming cleature
COCATION: (1937)...(1827)
OTHER RIPORANTOR: megAl. ACP1
NAME/KET: ming cleature
COCATION: (1937)...(2031)
OTHER RIPORANTOR: megAl. AT2
NAME/KET: ming cleature
COCATION: (1937)...(2031)
COCATION: (1937)...(2033)
                                                                                          INFORMATION: megAI, ACP-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION: (33052)...(33312)
THER INFORMATION: megAII, ACP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AME/KEY: misc feature
COCATION: (22318)...(22575)
THER INFORMATION: megAI, ACP2
                                                                                                                                  NAME/KEY: misc feature
LOCATION: (13849)...(15126)
OTHER INFORMATION: megal, KS1
                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (15427)...(16476)
OTHER INFORMATION: megAI, ATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AME/KEY: CDS
OCATION: (22867)...(33555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AME/KEY: misc feature
OCATION: (33052)...(3
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (15427)...(1
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TDP-4-keto-6-deoxyhexose 3,5-epimerase;
SBQ 1D NO: 8 translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             megG(megY), mycarosyl acyltransferase, mycarose O-acyltransferase
SEQ ID NO: 5= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCCATION. (Sa22)...(6595)
OTHER INFORMATION: megDII. daunosaminyl-W,N-dimethyltransferase (eryCVI homolog);
OTHER INFORMATION: 58Q ID NO: 7- translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              megBII-1(megDVII), TDP-4-keto-L-6-deoxy-hexose 2,3-reductase;
SEQ ID NO: 10= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: megBV, mycarosyl transferase, mycarose glycosyltransferase;
OTHER INFORMATION: SEQ ID NO: 11= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCRITON: (1)...(144)
OTHER INFORMATION: megEVI(megT), TDP-4-keto-6-deoxyglucose-2,3-dehydxatase;
OTHER INFORMATION: SBQ ID NO: 2= txanslated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      megDV, TDP-haxose 4-ketoreductase (eryBIV, dnmV homolog).
TDP-4-keto-6-deoxyMakose 4-ketoreductase;
SEQ ID NO NO: 9= translated anino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       megDII, deoxyaugar transaminase (erVCI, DnrJ homolog), TDP-3-keto-6-deoxyhexose 3-aminotransaminase; SEQ ID NO: 6= translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: meghl; SRQ ID NO: 13m translated amino acid sequence NAME/KEY (255)...(13470)
COCATION: (1255)...(13470)
OTHER INFORMATION: meghl, Ar-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         iccarrow (2072)...(3382)
OTHER INFORMATION: megDl, rhodosaminyl transferase (eryCIII homolog),
OTHER INFORMATION: TOP-megosamine glycosyltransferase,
OTHER INFORMATION: SEQ ID NO: 4= translated amino acid sequence
NOMENEX: CDS
LOCATION: 31462...(14544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (928)...(2061)
OTHER INFORMATION: magDVL, TDP-4-keto-6-deoxyglucose 3,4-isomerase,
OTHER INFORMATION: TDP-4-keto-6-deoxyhaxose 3,4-isomerase;
OTHER INFORMATION: SEQ ID NO: 3 = translated anino acid sequence
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TDP-4-keto-6-deoxyhexose 4-ketoreductase,
SEQ ID NO: 12= translated amino acid sequence
TYPE: DNA
PRANTSM: Micromonospora megalomicea
FERTURE:
NAME/REY: CDS
LOCATION: (1) ... (144)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. (5775)
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LOCATION: (6592)...(7197)
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TOCATION: (2072).
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... (45623)
: megCIII, desosaminyl transferase, desosamine glycosyltransferase;
: SEQ ID No: 17= translated amino acid sequence
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OTHER INFORMATION: megF, C-6 hydroxylase; SEQ ID NO: 20= translated amino acid seque
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; megalt. Z. degalll), TDP-4-keto-6-deoxy-L-glucose 2,3 dehydratase,
: TDP-4-keto-6-deoxyglucose 2,3 dehydratase;
: EDD 10 No: 18- translated amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COCTION: (165.01)... (165.91).

OTHER INPORMATION megall-12 (megall), TDP-4-Keto-6-decxy-L-glucose 2,3 dehydra
OTHER INPORMATION TDP-4-Keto-6-decxyglucose 2,3 dehydratase;
OTHER INPORMATION TDP-4-Keto-6-decxyglucose 2,3 dehydratase;
OTHER INPORMATION TDP-4-Keto-6-decxyglucose 2,3 dehydratase;
OTHER INPORMATION TDP-4-Keto-6-decxyglucose 2,3 dehydratase;
OTHER INPORMATION TDP-4-Keto-6-decxyglucose 2,3 dehydratase;
OTHER INPORMATION megH, TEII; SEQ ID NO: 19= translated amino acid sequence
NAME/KEX: OD:
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                       | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor; | NAME/KRY mas=factor;
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OTHER INFORMATION: megalii, ACPS
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December 5, 2003, 17:39:02 ; Search time 156:126 Seconds (without alignments) 7982-969 Million cell updates/sec Run on:

375
1 cctcccttccgagctgagc.....gaagccgccagccagaag 375 US-09-936-680-4_COPY_1_375 Title: Perfect score:

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Sequence:

2201672 seqs, 1661799599 residues Searched:

4403344

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Potal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

| Applied | Physical A | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Disposition | Dispo Published Applications NA:* Database :

Pred, No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution. SUMMARIES

		-de				
Result No.	Score	Query Match	Query Match Length DB ID	DB	ai.	Description
	375	100,0	1261	10	US-09-997-579-4	Semience 4. Appli
						THE PROPERTY
7	41.2	11.0		12	US-10-017-161-1435	Sequence 1435, Ap
m	41	10.9		10	US-09-771-161A-58	Sequence 58, Appl
4	41	10.9		10	US-09-771-161A-59	Seguence 59, Appl
v	40.2	10.7		11	US-09-291-417-102	Sequence 102, App
9	40.2	10.7		12	US-10-134-102-3	Sequence 3, Appli
7	39.8	10.6		10	US-09-960-352-2238	Seguence 2238. Ap
80	39	10.4	587	12	US-10-029-386-22980	Sequence 22980, A
σ	33	10.4		10	US-09-974-300-836	Sequence 836, App
0 10	38.6	10.3		12	US-10-029-386-24925	Sequence 24925, A
0 11	38.6	10.3		12	US-10-120-988-142	Sequence 142, App
12	38.4	10.2		12	US-10-017-161-1857	Sequence 1857, Ap
c 13	38	10.1	•	1	US-09-893-519A-87	Sequence 87, Appl
14	37.8	10.1	Ì	σ	US-09-899-634A-1	Sequence 1, Appli
15	37.8	10.1	4778	14	US-10-161-403-70	Sequence 70, Appl
16	37.8	10.1		11	US-09-954-483A-14	Sequence 14, Appl

Sequence 71, Appl Sequence 112, App	Sequence 127, App Sequence 126, App Sequence 13, Appl	Sequence 115, App Sequence 116, App Sequence 123, App		3, AE 1403, 1483,			Sequence 6888, Ap Sequence 20159, A Sequence 20159, A	Sequence 10338, A Sequence 10339, A Sequence 10340, A	Sequence 10338, A Sequence 10339, A Sequence 10340, A Sequence 38, Appl
US-10-161-403-71 US-10-161-403-112	US-10-161-403-127 US-10-161-403-126 US-09-954-4832-13	US-10-161-403-115 US-10-161-403-115 US-10-161-403-123	US-10-161-403-124 US-10-161-403-110 US-10-161-403-125	US-09-835-081-3 US-10-017-161-1403 US-10-017-161-1483	US-10-095-407-16 US-10-027-632-37453	US-10-027-632-37454 US-10-027-632-37453 US-10-027-632-37454	US-10-029-386-6888 US-10-027-632-20159 US-10-027-632-20159	US-10-027-632-10338 US-10-027-632-10339 US-10-027-632-10340	US-10-027-632-10338 US-10-027-632-10339 US-10-027-632-10340 US-09-927-827-38
7 7 7	11:	1777	144	127	122	222	222	222	2221
5855	6119	7600 7631 8521	9080 10474	57130 1117 3133	152331	412	531 779 779	1025	1025 1025 1025 2576
10.1	100	2000	1111	10.01	000		9 9 9	0,00	0000
37.8	37.8	37.8 37.8 37.8	37.8 37.8 37.8	37.8	37.2	37.	37 37	37	37 37 36.8
118	282	2222	26 27 27	23 30 30	3333	N W W	0 0 0 33 34 38 34	8 4 4 6 0 1	4 4 4 4 2 £ 4 5

ALIGNMENTS

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Parents of "Application U8/09997579

**Refers of "Application U8/09997579

**Refers of "U8/0000113703A,"

**GREAL HAPGMARITY Combridge University Technical Services

**TITLE OF HYMRHION: A novel family of Deta sub-unit proteins from a voltage gated s

**TITLE OF HYMRHION: A novel family of Deta sub-unit proteins from a voltage gated s

**TITLE OF HYMRHION: A novel family of Deta sub-unit proteins from a voltage gated s

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**TITLE OF HYMRHION: NOVEL STORY OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE OF TABLE 
JS-09-997-579-4
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Gaps ô Length 1261; Indels Query Match
100.0%; Score 375; DB 10;
Best Local Similarity 100.0%; Pred. No. 1.5e-93;
Marches 97; Conservative 0; Mismatches 0;

ORGANISM: Homo sapiens

US-09-997-579-4

LENGTH: 1261 TYPE: DNA

61 AAGCTGGAGTTCCGGGGTGGGCGGAGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGA 120 120 121 GCGGGCGCGCGCGCCTCGTCCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAG 180 61 AAGCTGGAGTTCCGGGGTGGGCGGGGGAGCGACTGTCCGTGGTGCTGACGCCGGCGGAGA à 쉽 ઠે ద à

121 GOGGGGGGGGGGGGGGGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAG 180

181 GOCCCOANGCCCCCAAAGCTCCAAAAGCTCCCAGGGCCTCCCAGGGCCTCCCAGGGCCCCGGGCCCCGGGCCCCGGGCCCCGGGCCCCGGGCCCC	; FEATURE: NAME/KEY: modified base 1 LOCATION: (142)(145)	· ů	: modified_base : (151) FORMATION: a, t, c,	FEATURE: NAME/CRI. modified_base LOCATION: (311) OTHER INFORMATION: a, t, c, g, unknown or other	FRATURE: NAME/KEY: modified_bage LOCATION: (322) OTHER INFORMATION: a, t, c, g, unknown or other. FEATURE:	; NAME/KEY: modified_base ; LOCATION: (326) ; OTHER INFRMATION: a, t, C, g, unknown or other sparing.	NAME/KEY: modified base 1 LOCATION: (345)(349) OTHER INFORMATION: a, t, c, g, unknown or other	FEATURE: NMME/KEY: modified_base LOCATION: (351)(361) OTHER INFORMATION: a, t, c, g, unknown or other	; FEATURE: NAME/KER: 1 NAME/KER: 2 NOCATION: (364) 2 OTHER INFORMATION: a, t, c, g, unknown or other	; FEMTURE: 1 NOME/CNE: 1 LOCATION: (366)(368) 2 OTHER INFORMATION: a, t, c, g, unknown or other	FEATURE: MANAFARION: (370)(380) COTHER INFORMATION: a, t, c, g, unknown or other	FEATURE: modified_base NAME/KEY: modified_base LOCATION: (384) OTHER INFORMATION: a, t, c, g, unknown or other	NAME/KEY: modified base 10CATION: (386)(388) COTHER INFORMATION: a, t, c, g, unknown or other FEAVURE:	; NAME/KEY: modified_base ; LOCATION: (332) ; OTHER INFORMATION: a, t, c, g, unknown or other ; FRANURE:	NAME/KEY: modified_base i_loCARION: (394)(396) COTHER INFORMATION: a, t, c, g, unknown or other FRAVURE:	NAME/KEY: modified_base LOCATION: (403) OTHER INFORMATION: a, t, c, g, unknown or other FEATURE:	. NAME/KEY: modified_base 	NAME/KET: modified base 1 LOCATION: (415)(417) COTHER INFORMATION: a, t, c, g, unknown or other FEATURE
SOS SOS SOS SOS SOS SOS SOS SOS SOS SOS	181 GGCCCAAAGCCCCACCCGGCTCCAAAAGCTCCCAGGCCTCCCCGGGGACCGGGACCTCCAAAAGCTCCCAAAAGCTCCCAAAAGCTCCCAAAAGCTCCCAAAAGCTCCCAAAAGCTCCCAAAAGCTCCCAAAAGCTCCCAAAAAGCTCCCAAAAAGCTCCCAAAAAGCTCCCAAAAAGCTCCCAAAAAGCTCCCAAAAAGCTCCCAAAAAGCTCCCAAAAAAGCTCCCAAAAAAGCTCCCAAAAAAGCTCCCAAAAAAGCTCCCAAAAAAAGCTCCCAAAAAAAA	241 GCCCTTCCTTCGGTCAGANGTCGCCCCTGGGGGAGTTCGTCCCANAGGGTTCCTCG	301 AAAGAATCTGAGAGGGGGAGTCCTTGACGGAGGAATCTCTCTGTGAGCCTTGGAGG	361	RESULT 2 18-10-017-161-1435 7 Sequence 1435, Application US/10017161	PUDICACTION NO. 22003014368A1 APPLICANY: SINAM, MAXIZO APPLICANY: SINAM, MAXIZO	APPLICANY: AKTWAM, YUDAX APPLICANY: AKTWATANI, HENCUKI TITLE OF INVARIANISH HOVEL G PROTEIN-COUPLED RECEPTORS	CURRENT APPLICATION NUMBER: US/10/017,161 PRIOR RELING DATE: 070-12-18 PRIOR REPUBLICATION NUMBER: UP 200/1446799	WINNER OF DE SO THE SO	TIPE: DWA TIPE:	LOGATOR: (201) LOGATOR: (1)(92) FEAVURE: (1)(92) NAME/EXT. (201) COCATOR: (201)(722)	ů	ű	c, g, unknown or	modified base: (127)(128) FORMATION: a, t, c, g, unknown or	modified_base: (131) PORMATION: a, t, c, g, unknown ox	modified base: (133)(134) FORMATION: a, t, c, g, unknown or	NAME/KEY: modified_base UCMATION: (138) OTHER INFORMATION: a, t, c, g, unknown or other

Gaps

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61 AAGCTGGAGTTCCGGCGTGGGCGAGGCGACTGTCCGTGGTGCTGAGCGCCCGGCCAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 écéccioscricososcriens Acceserres descricos de consecuencios de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecuencias de consecu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 GCCGGCCGGAGTTGCCTCCCGGGGCCCGCGCTGAGGCCCCGCCGCCGCCGCCT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 GCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAGGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 922;
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10.3%; Score 41; DB 10; Length 1097; Bert Local Similarity 52.0%; Pred; No. 0,053; Matches 92; Conservative 0; Matches 85; Indela (Matches 195); Conservative 0; Matches 195; Indela (Matches 195); Conservative 0; Matches 195; Indela (Matches 195); Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Matches 195; Match
                                                                                                 Ouery Match 11.0%; Score 41.2; DB 12; Length of the Coal Similarity 40.9%; Fred. No. 0.047. Matches 70; Conservative 0; Mismatches 101; Indels Matches 70; Conservative 0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/0971161A

REMEM, MARGAMOTOLIGIAL

APPLICAMY LEVINES
FILE SET LEVENTION, UNELTANCE OF PROTEIN KINASES
FILE REPRENCE: 802-2016-1

CURRENT APPLICATION NUMBER: US/09/771,161A

CURRENT PILING DATE: 2000-10.26

PRIOR PILING DATE: 2000-11.28

PRIOR PILING DATE: 2000-01.28

PRIOR PILING DATE: 3000-06-15

PRIOR PILING DATE: 3000-06-12

RANGER OF SEQ ID NOS: 273

SOFTAMES RefearIn Version 3.0

SOFTAMES RefearIn Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT. 613-59
| Sequence 53 Application US/09771161A |
| Sequence 54 Application US/09771161A |
| Sequence 55 Application US/09771161A |
| CONTROL INFORMATION UNITS |
| TITLE OF INVENTION UNITS |
| FILE REFRENCE: 80260-2005.1 |
| PLICE REPRENCE: 80260-2005.1 |
| PRICE REPLIES DATE: 2001-01-26 |
| PRICE RELING DATE: 2001-01-28 |
| PRICE RELING DATE: 2001-11-28 |
| PRICE RELING DATE: 2001-11-28 |
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US-09-771-161A-58
        LOCATION: (573)
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                                                                                                         g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (487)..(488)
JTHER INFORMATION: a, t, c, g, unknown ox other
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LOCATION: (490)..(491)
OTHER INFORMATION: a, t, c, g, unknown or other
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OCATION: (497)..(498)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (501).. (505)
OTHER INFORMATION: a, t, c, g, unknown or other
FRATURE:
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OTHER INFORMATION: a, t, c, g, unknown ox other
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LOCATION: (564)..(568)
OTHER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
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LOCATION: (469)..(471)
JTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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MANEKEY: modified base
LOCATION: (548)..(549)

OTHER_INFORMATION: a, t, c, g, unknown
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LOCATION: (529)..(530)
OTHER INFORMATION: a, t, c,
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THER INFORMATION: a, t, c,
                                                                                                         DITHER INFORMATION: a, t, c,
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BOCATION: (540)

THER INFORMATION: a, t,
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LOCATION: (445)
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LOCATION: (465)
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| GENERAL INFORMATION No. US20318625431
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| CURRENT APPLICATION NUMBER: 08/10/134,102
| PRIOR ELLINO DATE: 2002-04-29
| PRIOR ELLINO DATE: 200-04-29
| PRIOR ELLINO DATE: 399-12-30
| WUMBER OF ERQ IN MOS: 10
| SOFTWARE PARCED. TO MOS: 10
| SOFTWARE PARCED. TO MOS: 10
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10.7%;
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LOCATION: (211)..(1986)
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ORGANISM: Homo sapiens
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ORGANISM: Bos taurus
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; OTHER INFORMATION: "n" can be any nucleotide 'a', 'c' , 'g' or 't'
5 OTHER INFORMATION: "n" can be any nucleotide 'a', 'c' , 'g' or 't'
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REBLICATION NO. RESEARCH TOWNS OF THE SEGUENCE TO THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF THE SEGUENCE TOWNS OF
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1 ORGANISM: Full Length Mammalian (Human) PAKS
17-09-291-417-102
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                                                PRIOR APPLICATION NUMBER: 135619
FRIOR FLITAM DATE: 2000-04-12
NUMBER OF SEQ 1D NOS: 273
SOFWARE: PatentIn version 3.0
SEQ ID NO 9382
LENOTH: 3382
PRIOR FILING DATE: 2000-06-15
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Matches 92; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Parm, Sharron G.
APPLICANT: Parm, David R.
TITLE OF INVESTION: THORAL, DESCRIPTION SINGLE EXON NUCLEIC ACID PROBES USBEUL FOR TITLE OF INVESTION: EXPRESSION MALYSIS TWO
TITLE OF INVESTION: EXPRESSION MALYSIS TWO
FILE MEPRINCE: ADMINISTRY OF ALCALION NUMBER: USJ.04/029,386
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.65
OTHER INFORMATION: FAISSPROT HIT 035052, EVALUE 4.00e+00
OTHER INFORMATION: MTH.: $115505052, EVALUE 5.20e+00
OTHER INFORMATION: BETS_TURAB HIT: BFT484543, FVALUE 1.00e-103
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Publication No. US20030194704A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              Sequence 836, Application US/09974300 patent No. US20020146721A1 GENERAL INFORMATION:
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LOCATION: (1)...(936)
OTHER INFORMATION: n = A,T,C or G
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US-10-029-386-24925/c
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OTHER INCORPORTOR: EXCRESSED IN BRAIM, SIGNAL = 1.5
OTHER INCORPORTION: EXCRESSED IN DUNG MARROW, SIGNAL = 1.0
OTHER INCORPORTION: EXCRESSED IN DUNG MARROW, SIGNAL = 1.0
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OTHER INCORPORTION: SET MAISSENGE II FT: P19332 ENALURE 2.700+00
OTHER INCORPORTION: SET MAISSENGE II FABLURE 2.700+00
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48.7%; Pred. No. 0.19;
tive 0; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 GGTCCAGTGGGGTCGCTTAGGGCCCCAAAGCCCCCCAACCCCGGCTCC 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 greccacedadescecerrecessecessacecesceces
; OTHER INPORMATION: unsure at all n locations Us. OTHER INPORMATION: Clone ID: 10-LIB3058-057-Q1-K1-C5 US.09-960-582-2238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: MAP TO AL035703.17
OTHER INFORMATION: EXPRESSED IN HELA,
OTHER INFORMATION: EXPRESSED IN BRAIN,
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Matches 135; Conservative
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NAME/KEY: modified base
LOCATUR: (658)..(669)
OTHER INFORMATION: a, t, c, g, unknown or other
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OCCATION: (739)..(743)
TTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
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LOCATION: (745)..(747)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (671)..697)
JTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (704)..(707)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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PATHER INFORMATION: a, t, c, g, unknown or other
PATHURE:
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STHER INFORMATION: a, t, c, g, unknown
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NAME/KEY: SOURCE
LOCATION:
FRATURE:
FRATURE:
LOCATION: (201) .. (2963)
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LOCATION: (556)..(655)
OTHER INFORMATION: a, t,
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LOCATION: (761)
OTHER INFORMATION: a, t,
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OTHER INFORMATION: a, t,
FEATURE:
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LOCATION: (754)..(756)
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ORGANISM: Homo sapiens
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                                                                                                                       y Match 10.3%; Score 38.6; DB 12; Length 550; Lbcal Smilarity 52.9%; Pred 100.025; D52 Smilarity 52.9%; Pred 100.025; D53, Conservative 0; Mismatches 74; Indels 0, the 33; Conservative 10; Mismatches 74; Indels 0,
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Sequence 1857, Application US/10017161
Publication No. US70030143668A1
APPLICANT: GUN, MAKITO
APPLICANT: ASAI, KTYOSHI
APPLICANT: AKITAMA, YUTAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 142, Application US/10120988
Publication No. US2020219745A1
GENERAL INFORMATION
APPLICANT: TOMA
APPLICANT: GOODICAL, RVIe
APPLICANT: Liu, Chenghua
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Matches 83, Conservative
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; LOCATION: (1)..(1374)
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US-10-017-161-1857

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2183 GGGGGGGGGGGGGGGGGGGGNNNGGGGG 2217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified base
LOCATION: (1968). [1980)
OTHER INFORMATION: a, t, c, 9, unknown or other
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1866). [1965)
OTHER INFORMATION: a, t, c, 9, unknown oz other
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Publication No. US0030027743A1
GENERAL INFORMATION:
RAPLICANT: ANADISS PHARMACEUTICALS, INC.
APPLICANT: THOMPON, CAA'G
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LOCATION: (1982)..(2009)
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LOCATION: (1105)..(1107)
JTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1247)..(1248)
OTHER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1066)..(1067)
OTHER INFORMATION: a, t, c, g, unknown or other
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ATION: (1082)..(1084)
ER INFORMATION: a, t, c, g, unknown or other
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HER INFORMATION: a, t, c, 9, unknown or other
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ER INFORMATION: a, t, c, g, unknown or other
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LOCATION: (1485)
OTHER INFORMATION: a, t, c, g, unknown or other
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OTHER INFORMATION: a, t, c, g, unknown or other
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ER INFORMATION: a, t, c, g, unknown or other
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ER INFORMATION: a, t, c, g, unknown or other
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NAME/KEY: modified base
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Pacent No. US/0102005564A
Except No. US/0102005564A
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Query Match

10.1%; Score 36; DB 11; Length 2307;

Best Local Similarity 56.3%; Pred; No. 0.34%; One

Matches 71; Ognesrvative 0; Missacches 55; Indels

Matches 71; Ognesrvative 0; Missacches 55; Indels
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TITLE OF INVENTION' NUTERIOGL COMPOUNDS AND METHODS OF USE
TITLE OF INVENTION' NUTERIOGL COMPOUNDS AND METHODS OF USE
TITLE OF INVENTION' NUTERIOR OF 0993,519A
CURRENT PELLING DATE: 200.-06-29
TROOR PELLING DATE: 200.-06-29
PRIOR PELLING DATE: 200.-06-29
PRIOR PELLING DATE: 200.-06-29
PRIOR PELLING DATE: 200.-06-30
PRIOR PELLING DATE: 200.-06-30
PRIOR PELLING DATE: 200.-06-30
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DATABASE ACCESSION NUMBER: Human Genbank/Y11354.1
DATABASE BRIEV DATE: 1997-06-25
RELEVANT RESIDUES: (1)..(2307)
MOORE, Jeffrey
BURMAN, Ed T.
BRADLEY, John
DESILVA, Thamare
HARRIS, Sandma
KOMARNITSKY, Svetlana
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SOFTWARE: PatentIn version 3.1
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MOORE, Daniel
MCCOY, Melissa
SANDERSON, Karen
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US-09-899-634A-1
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ZHU, Shuhao
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ORGANISM: porcine
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ilarity 50.3%; Pred. No. 0.37;
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APPLICART: Pleming, Blona
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CURRENT APPLICATION NUMBER: 105/10/151,403
CURRENT FILING DATE: 2002-05-30
PRIOR PALLIANTON NUMBER: 60/759,738
PRIOR PALLIANTON NUMBER: 60/759,738
PRIOR PALLIANTON NUMBER: 60/759,738
PRIOR PALLIAN DATE: 2001-05-30
PRIOR PALLIAN DATE: 2002-03-21
WUMBER: 05 REQ ID NOSE: 129
SOFTWARE: FastSOF for Mindows Vorsion 4.0
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Publication No. US203030119104A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward
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Lindenbaum, Michael
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Leung, Josephine
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Best Local Similarity
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Job time : 157,126 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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5, 2003, 14:16:11; Search time 993.523 Seconds (without alignments)	9799.969 Million cell updates/sec
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Run on:	

Title:	US-09-936-680-4_COPY_1024_1261
Sequence:	1 aacaggagcagtagacatgtgccagaactgagaagcegg 238
Scoring table: IDENTITY_NUC Gapop 10.0 ,	IDENTITY NUC Gapop 10.0 , Gapext 1.0

Gapop 10.0 , Gapext 1.0 Searched: 2889711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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sodium channel that modulates channel gating with distinct Kinetics
Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifies
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Homo sapiens (human)
Homo sapiens
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100.0%; Score 238; DB 6; Length 1261;
Bert Local Similarity 100.0%; Pred. No. 2.78-59
Matches 238; Conservative 0; Mismatches 0; Indels 0;
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                                                                              Services Limited (GB)
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Bikkaryofe's Wiensans; Concadest, Crematist; Wertebrotes, Burelsoctomi; Mananais Butherisa Permates; Catarthin; Hominidae; Homo.

1 Deages 1 to 127347; Mananais Catarthin; Hominidae; Homo.

Philyman, A. Yada, T. Torocki, Y. Watarabe, H. and Sakaki, Y. Homo eapiens 117, 347 genomic DBA of 11244. And Andreade only in Deages (11247). Proposity A. Torocki, Y. Watarabe, H. and Sakaki, Y. Homo eapiens 117, 347 genomic DBA of 11245. The Proposity A. Torocki, Y. Watarabe, H. and Sakaki, Y. Homo eapiens 117, 347 genomic DBA of 11245. The Proposity A. Torocki, Y. Watarabe, H. and Sakaki, Y. Dirister, Subhitzed (1280) yasanira a Hattori, The Institute of Physical and Chemical Research (RIKBN) Genomic Sciences Center (GSC); Andreade (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC) and Catarabe (GBC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 696 AACAGGAGCAGTGTGACATGAGGCCTTGAACACCTGAGGGACTGGACATCCCATGTTC 755
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Start codon is not identified."
                                                                                                                                                                                                                      /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
1. .5306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 9.6e-59;
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       organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA86472.1"
/db_xref="GI:6330136"
                                                   /mol_type="mRNA"
/db xref="taxon:9606"
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Homo sapiens (human)
Homo sapiens
                                                                                                                                            /clone="hj00081"
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Direc Subaisson.
Submisson February S. Sanda Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obara Obar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1512 AGCAATGTCAATGGCATCAGGAGGGGGCCCCAAGGGCCCCATGGCTTCCCTTCATGCATC 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 11-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CATTGITCTGITCATTCATTCATCCATACATCCACCTGCCTCTGAGCTTTCACCTCTGAC 180
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DNA mise-Eractionated CONN libraries from human brain
DNA Res. 5 (5), 325-336 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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182 TCCCTTAACTCAATCAGACTCTAGGACATAAGACTGTGCCAGAACTGAGAAGC 1897
/tissue_type="amygdala"
|Colone_lib="761 (8ynonym: hamy2), Vector pSportl; host
| DH108; sites Not! + $all"
| /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AACAGGAGCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%; Score 236; DB 9; Length 4052; 100.0%; Pred, No. 9.8e-59; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB032984 S306 bp mRNA linear 1
Homo sapiens mRNA for KIAA1158 protein, partial ods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein id="CaB66524.1"
/db_xref="G1:13276681"
                                                                                                                                                                                                                                                                                                                                                                          note="scn3b (Homo sapiens)"
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                                                                                                                                                                                                                                     gene="DKFZp761F182"
                                                                                                                                                                                                                                                                                                                              'gene="DKF2p761F182"
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1. .5306
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Homo sapiens
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Natches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       994 a
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VERSION
KEYWORDS
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TITLE
JOURNAL
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BURANCHAR Medason Chordata, Cranista, Vertebrata, Butelsoetomi, Bukanchas, Primates, Carterfini, Meninidae, Mono.

Rammalia, Buthoria, Primates, Carterfini, Genan, R. A. Allan, C. Markey, M. Adeas C. Adio-Cholda, B. Ali coman, R. M. Adeas C. Adio-Cholda, B. Ali coman, R. M. Adeas C. M. Adeas, M. Markey, M. Adeas C. Adio-Cholda, B. Ali coman, R. M. Markey, T. Markey, C. Barret, S. Mancher, S. Markey, C. Barreth, R. Mancher, T. Markey, C. Barreth, R. Market, C. Burreth, K. Market, C. Market, C. Market, M. Byrd, N. C. Chan, G. Chen, G. Chon, G. Chen, G. Chon, G. Chen, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chen, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon, C. Chon
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/note="assembly_fragment"
112414. .121043
https="assembly_fragment clone_end:T7 vector_side:right"
121144. .125917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCAG 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.8%; Score 216; DB 2; Length 127347; 100.0%; Pred. No. 6.1e-53; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                          700 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 CTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 236
                                                                                                                                                                                                                            /note="assembly_fragment"
misc_feature 126018 1.27374 fragment"
/note="assembly_fragment"
BASE COUNT 36325 a 27508 c 27825 g 34989 t
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Homo sapiens (human)
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Matches 216; Conservative
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                                                                         misc_feature
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                  Center: RIKEN Genomic Sciences Center (GSC)
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Cobract: hattor/@gsc.it/ken.go.jp
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Gaps

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Service B. Litton I. V. Mastan, C. Lander, E. Abraham, H., Allen, N., Anderson, S. Baldein, J., Barra, M., Beckerly, R., Beda, F. Anderson, S. Baldein, J., Barra, M., Beckerly, R., Beda, F. Changelo, M., Colling, S., Collymore, A., Cooke, P., Choepel, Y., Collangelo, M., Colling, S., Collymore, A., Cooke, P., Perreitze, P., Firtheld, M., Forrest, C., Gage, D., Gallagan, J., Ferreitze, P., Firtheld, M., Forrest, C., Gage, D., Gallagan, J., Ferreitze, P., Firtheld, M., Forrest, C., Gage, D., Gallagan, J., Karata, C., Gage, B., Machan, J., Karata, A., Klein, R., Medan, J., Karata, M., Medan, R., Karata, M., Medan, R., Medan, M., Wederne, R., Medan, M., Medan, D., Mochi, M., Wederne, R., Medan, M., Medan, D., Mochi, M., Welsen, M., Pistani, C., Pollazza, V., Raymond, C., Rilay, R., Rothman, D., Ferreitz, M., Sahron, R., Severy, September, B., Stanger, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, T., Chang, D., Sahron, D., Sahramanian, A., Falana, J., Tesfaye, S., And, Sahrilaw, H., Viel, R., Vo, A., Wu, X., Waman, D., Ye, W.J., Rimer, A., and Szoly, M., Mu, X., Waman, D., Ye, W.J., Rimer, A., and Szoly, M.
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Mammalia, Butheria, Primates, Cararthini, Hominidae, Homo.
I (Dases I to 14980)
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      $553 $565; contig or 12666 bin length $657 $776; app of unknown length in $777 $1300; contig of 12553 bin length $1310 $1340; app of unknown length in $1310 $1357; contig of 25848 bp in length $185 $11397; gap of unknown length in $1557; gap of unknown length in $1557; gap of unknown length in $1558 $14331; contig of $2876 bp in length.
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/db_xref="taxon:9606"
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Matches 216, Conservative
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Rang, S., Ward-Noore, S., Warren, R., Washington, C., Warlington, S.,
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Walless, G., Willinson, A., Wieczyk, R., Wooden, S., Worley, X.,
Wanner, G., Wall, T., Zhou, J., Zorrilla, S., Walson, D.,
Wanner, G., and Gibbs, R.
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Submitted (22-Apr. 2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plasa, Houston, TX 77030, USA
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: gtc-seqcenterSenomecorp.com
Context: gtc-seqcenterSenomecorp.com
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Homo sapiens (human)
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Tel:81-42-778-9923, Fax:81-42-778-9924)
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E. Z. (bases I to 17816)

Hattori, M., Ishii, K., Toyoda, A., Taylor, D., Hong-Seog, P., Philyson, A., Yadai, T., Toyoda, A., Taylor, D., Hong-Seog, P., Differ, Sonnisaion, 2000, Masaki, H. and Sakaki, Y. Differ, Sonnisaion, 2000, Masaki, H. Hattori, The Intitute of Physical and Chamacoll Beastrol (Rixshi, Georgic George Construction of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Constructions of Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physical Physi
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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MMYILLYPITJALLLEBATYCYRKVGSKABBAAQBKASDYLA,TBSBKRISAVPREF
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(protein_id=BACA1446.1*
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                         AB097521 A296 bp mRNA linear PRI 06-DEC-2002 Macaca fascicularis brain cDNA clone:QmoA-13657, full insert
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Submitted (05-ERC-2002) Katenyuki Hashinoco, Mational Institute of
Infection Diseases, Division of Genetic Resources, 23-1, Toyama
Infection Shinjuku-ku, Toyyo 162-8640, Japan
(6-mail/Abshidmail. Apol. Dy URL, 190-19, Parish 3-538-1181)
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                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutherisa, Primares, Catarrhini, Cercopithecidae, Medoa.
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Seco,Y., Hiral,M., Terack,K., Suzuki,Y., Sugano,S. and Habihaco,K.
Sesigment of 118 novel offske of cytomologus monkey brain to human
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
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/clone lib="macaque brain cDNA library QmoA"
/dev stage="adult"
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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59155 CATCCATACATCCACCTGCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCAGACCT 59096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (123-ARR-2002) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, Mr Od45s, USA on Apr 23, 2002 this sequence version replaced gi:10881056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Simbinsision Direct Simbinsision Submitted (02-UNR-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 0753, USA 105 Noses 1 to 181471
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1. (hases, 1 to 181471)
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61 AGCAATGTCAATGGCATCAGGAGGGCGCCCAAGGGCCCCATCGCTTCCTTTCATGCATC 120

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On Nov 13, 2002 this sequence version replaced gi:2515924.

The sequence of this sequence or combination of Baylor Based reads and whole genome shorgun sequencing reads assembled using A.Lisa in the Facture table below registrating as seal control described in the Results table. Denitor represents a socificial in the A.Lisa in the Facture table below registed and crimendes and separated by discal gaps filled with Ns to the setting size. The sequence contriger within a contriger-coaffold that consists entirely of whole genome shorgun sequence cands. Both end sequences and whole genome sincepum sequence only yourly set will be indicated in the feature
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhauscrn,A., Weise,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock, G. and Gibbs,R.A.
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7765. .9270
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163751: gap of 100 bp
165586: contig of 1885 bp in length
165736: gap of 100 bp
167342: contig of 1606 bp in length.
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of 6692 bp in length
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTGITCIGTICATTCATTCATCATCATCCACCTGCCTCTGAGCTTTCACCTCTGAC 180
                                                                                                                                               Novel sub-unit for voltage-gated sodium channel proteins for producing agents useful for treating pain
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                                                     Sanseau P;
                                                                                                                                                                                                     Claim 4; Page 29-30; 31pp; English.
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                                                              Novel nucleic acids encoding a beta-3 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, usefall for detecting and treating sodium channel-associated conditions, e.g. pain,
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Local Similarity 100.0%; Pred. No. 2e-69;
es 238; Conservative 0; Mismatches 0;
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1452 AACAGGAGCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTC 1511
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                                                                                                                 The present invention describes essemblages and computer readable media comperizing proval human cDNA sequences and clones detrived from human forth sequences and clones detrived from human flowers. Edetal Kindry, maintained, restricted and saydable CDNA illibraries. ABA93702 to ABA93766 represent human CDNA sequences from the present invention which encode the proceins given in ABB05662 to ABB0529. The human CDNA sequences and clones can be used in gene cample they may be used in profiling assays, for applications, for example they may be used in profiling assays, for providing large arrays of human genetic meterial for implementing large-scale screening strategies and for Incanting diseases via gene therapy procedures.
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             Human cDNA sequences and clones derived from human fetal brain, fetal kidney, melanoma, testis and amygdala cDNA libraries, useful in genetic
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                                                                                   Claim 1; Page 174-175; 611pp; English
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AGGTGGCCTGAACACCTGAGGGACTGGACATCCCCATGTTCAGCAATGTCAATGGCATCAG 21 AGGIGGCCIGAACACCIGAGGGACIGGACATCCCAIGITCAGCAAIGICAAIGGCATCAG

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The present invention provides the protein and coding sequences of a number of human reproductive system related anyigns. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a process of the invention.
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2000US-0241808.
2000US-0241809.
2000US-0244617.
2000US-0246477.
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|Muman, testivultar antigan; testes; acnoer; mestestesis; ammune disorder; sepreductive pystem disorder; urinary system disorder; pene therapy; aspraionacultive pystem disorder; pene therapy; aspraionacultive special disorder; gene therapy; aspraionacultive processing disorder; gene therapy; aspraionacultive processing disorder; gene disorder; gene processing disorder; gene processing disorder; gene processing disorder; gene processing disorder; gene processing disorder; gene processing disorder; gene processing disorder; gene processing disorder; gene processing disorder; general

17-JAN-2001; 2001WO-US01329

WO200155317-A2.

02-AUG-2001.

domo sapiens.

Human testicular antigen encoding DNA fragment SEQ ID NO: 2516

(first entry)

21-JUN-2002

ABL97864;

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72-1848-2000; 2000018-018-955

17-1848-2000; 2000018-018-955

17-1848-2000; 2000018-019-912-1

19-1848-2000; 2000018-019-912-1

19-184-2000; 2000018-020-9515-1

19-184-2000; 2000018-020-9515-1

19-184-2000; 2000018-021-95-1

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2000US-0180628.
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2000US-0225758.
2000US-0225759.
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14-AUG-2000; 2
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DB 22; Length 4625;

Sequence 4625 BP; 1222 A; 1130 C; 906 G; 1367 T; 0 other; 90.8%; Score 216;

Query Match

2000US-0226281 2000US-0226681 2000US-0226681 2000US-022681 2000US-02270182 2000US-02270182 2000US-022944 2000US-022944 2000US-022944 2000US-022944 2000US-0229143 2000US-022144 2000US-022144 2000US-022144 2000US-022144 2000US-022144 2000US-022144 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143 2000US-022143	80000000000000000000000000000000000000	\$1000 \$1000
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81 GAGGGGCCCCAACGCTTCCCTTCATGCATCCATTGTTCTTCATT 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides the procein and coding sequences of 973 human testicular antiques, and fragements of their genomic sequences. The sequences can be seed in the treatment of cardiovascular, urinary system, respondences can be system, minimar, respiratory, meurological and system, system, respondences in the present sequence is a man or especially cardious. Infections, infections, especially cancer, proceeding the present sequence is a DNA encoding a protein fragment of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
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90.8%; Score 216, DB 23;
Best Local Similarity 100.0%; Pred. No. 7.88-62;
Matches 216; Conservative 0; Mismatches 0;
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          17-RNV-2000) 200008-043970
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213 CTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 248

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17-NOV-2000; 2
17-NOV-2000; 2
    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34465.
                                                    AAK79653 standard; DNA; 11089 BP
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2000018-0215115
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2000US-0229509.
2000US-0229513.
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2000US-0231413.
2000US-0231414.
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                                                                                             07-NOV-2001 (first entry)
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08-SEP-2000;
08-SEP-2000;
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                                                                        AAK79653;
                                          AAK79653
ID AAK
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the present investion describes an isolated egenomic polymuclastide (1), which is obtainable from the pis region of human chromosome 11. (1) the pis selection of the pis region of human chromosome 11. (1) the pis selection of the pis region of the pis region of human chromosome 11. (1) the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selection of the pis selectio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conditions. These conditions include tumour growth, infertility, or negatitis C virus infection.
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0; Mismatches
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ID ABK64794 standard; DNA; 3768
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Best Local Similarity 62.81
Matches 59; Conservative
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                Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, especial for preventing, diagnosing and/or treating cancers and metastasis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I)
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17-807-2009, 2000HS-0249100, 101-BEC-2000, 2000HS-0250160, 101-BEC-2000, 2000HS-025139, 105-BEC-2000, 2000HS-025139, 105-BEC-2000, 2000HS-025139, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025146, 106-BEC-2000, 2000HS-025146, 106-BEC-2000, 2000HS-025146, 106-BEC-2000, 2000HS-025146, 106-BEC-2000, 2000HS-025146, 106-BEC-2000, 2000HS-025148, 106-BEC-2000, 2000HS-025148, 106-BEC-2000, 2000HS-025148, 106-BEC-2000, 2000HS-025148, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2000HS-025149, 106-BEC-2000, 2
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05-JAN-2001; 2001US-0259678.
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The invention relates to a method of disposition (11) for controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controlled controll
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression lavels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate
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                                                                                      07-AUG-2001, 2001WO-US24708.
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                                                                                                                                                                                                                                                                             (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                                                                                                                       Kulkarni P,
                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC.
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15.9%; Score 37.8; DB 24; Length 3768; 60.0%; Pred. No. 0.039; tive 0; Mismatches 42; Indels 0;
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Human; cancer; colon; breast; ovary; ossophagus; kidney; thyroid; sconed;, lung; prostate; parcreas; ordinoma; antithemour; adencezoinom; cyrostatic; gene therapy; antineoplastic; Milm's tumour; adencezoinoma; Breast cancer related gene sequence SEQ ID NO:1231. ABL62894 standard; DNA; 3768 BP 15-MAY-2002 (first entry) ABL62894; ABL62894/c

MARKEY PARKE

RESULT

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25-38P-2000; 2000US-234567P.
25-88P-2000; 200US-24923P.
25-88P-2000; 200US-249247P.
25-88P-2000; 200US-235007P.
25-88P-2000; 200US-235304P.
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CG-CGT-2000 20000G-277234

CG-CGT-2000 20000G-277356

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22-SEP-2000; 2000US-234509P-
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                 Homo sapiens.
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(AVAL-) AVALON PHARM.

Endress G, Horrigan S; Carter KC, Ebner R, Augustus M, Weaver Z; WPI; 2002-188264/24. Soppet DR, foung PE,

Screening for anti-neoplastic agent involves exposing cells to a descript agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set Claim 1; SEQ ID 1231; 44pp; English

The present invention describes a method (MI) for screening for an auti-mochlatic describer he method involves expessing cells to a chemical agent to be tested for anti-mochlatic activity, determining a change in expression of a talest one upon (I) of a signature gene each, where (I) comprises a sequence (S) selected from 647 sequences (given in Asiacises (COMINIO) or Is at less 19% identical to (S), where a change in expression is indicative of anti-mochlatic activity. (I) has opposed to

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105 CTTCCCTTCATGCATCCATTGTTCTTCATTCATTCATCCATACATCCACCTCTG 164
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activity and can be used in gene therapy, Mr can be used for screening in anti-troopbarie agents which in anti-troopbarie agents with a new for the production agents with result of ML, and the data is sufficient to convey the chemical a structure and/or properties of the agent, Mr can be used in the treatment of cancer such as colon, breast, stomeon, lung, thyroid, casophageal, ovarian, McHany, proster or pancreatic cancer in Militaria adenocations, class call cancer, infiltrating duct, adenocations, class call cancer, infiltrating duct, and cancer, and conserved to the conserved cancer and will be a colon, breast, and conserved the cancer and will be a colon and will be a colon and will be actioned.
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stomech; gene therapy; antineoplatic; Milm's tumour; adenocarcinoma;
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anti-inexplastic agent. The method involves exposing cells to a chemical anti-inexplastic agent. The method involves exposing cells to a chemical anti-inexplastic agent. The method involves exposing cells to a chemical expression of at least one gene (1) of a signature gene set, where (1) conceptses a necession of at least 54 identical to (8), where a change in concepts a necession is influente of a net inexplastic activity. (1) has organized to ABIVIDIO, or is at least 55 identical to (8), where a change in the expension is influente of anti-inexplastic activity. (1) has organized and one be used in gene therapy. Mr can be used for correcting a strict incorporate and one to use and the properties of the seent. Mr can be used in the creating of treatment of an Tomber of the seent. Mr can be used in the creatment of cancer such as orlon, breast, stometh, lung, thyroid, adeptocation and/or properties of pancessic cancer, stomethy and the control of the seent of pancessic cancer.

The second of the control of the seent of pancessic cancer, adeptocation of adeptocations of actions and white of cancer will interacting quick a cancer will cancer a general cancer. The second of the sections and while the cancer will be cancer will be a cancer will be cancer will be a cancer of pancessic and the cancer will be cancer will be cancer will be cancer.
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0; Mismatches 42; Indels
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                                    2000US-236891P.
2000US-237172P.
2000US-237173P.
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2000US-236842P
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous; cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
                cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 Prostate cancer related gene sequence SEQ ID NO:7935,
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                                                           Homo sapiens.
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                 Human;
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Horrigan S; Endress G, Ebner R, "PI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a otherwisel agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set Claim 1; SEQ ID 7935; 44pp; English. The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical

Security to be tested for anti-inoplastic exceptivity, determining a change in expression of at least one gene (1) of a signature gene set, where (1) of comprises a sequence (s) set-feted firm shall add to sequence (s) where a change in comprises a sequence (s) and the set of set least 584 identical to (6), where a change in the compriser of set in the set of set of set of set least 584 identical to (6), where a change in the set of ö 1112 carccorrearecarecarecereceretarecereceretareceretarecerecere 105 CTTCCCTTCATGCATCCATTGTTCTTTCATTCATCCATACATCCACCTGCCTCTG 164 Gaps ö DB 24; Length 3768; 1052 Arcarccrccrccarccarcrarccarcarcacccarc 165 AGCTITCACCTCTGACTCCCTAACTCCATCAGACCTCTACGCACC 209 Indels Sequence 3768 BP; 1030 A; 730 C; 1089 G; 919 T; 0 other; 3; 0.039; 42; Pred. No. 0.03 0; Mismatches ch 15.9%; Score 37.8; 1 Similarity 60.0%; Pred. No. 0.0 63; Conservative 0; Mismatches Local Similarity Query Match Matches 888888888888888888888 쉺 ð

N. meningitidis partial DNA sequence gnm_220 SEQ ID NO:220. AAA81673 standard; DNA; 1367 BP 04-DEC-2000 (first entry) AAA81673; AAA81673

Neiseria meningitidis, Neisseria gonorrheae; genome; immunogenic; antigen, vaccine; diagnosis; infection; antibacterial; identification; Meningococcus B; MenB; ds. 99WO-US23573.. Neisseria meningitidis. WO200022430-A2. 08-OCT-1999; 20-APR-2000.

Tettelin H, Venter JC; Ratti G, Scarselli M, Peterson J, C, Mora M, 98US-0103794. Hickey E, Galeotti V, Gateur (CHIR) CHIRON CORP. 09-0CT-1998; 30-APR-1999; Rappuoli R, Frazer CM,

Scarlato V;

toolsted mucleotide sequences of Neigearia meningitidis which can be used in the disaposis and treatment of N. meningitidis infection and other Neigearia infections, for example, N.gonorthosa.

WPI; 2000-318079/27.

Claim 7; Page 1535; 1760pp; English.

The present invention describes methods of obtaining immunogenic proteins from Neisseria agenomic sequences. AAABA145 to AAABA214 represent poscifically claimed Neisseria meningitidis genomic DNA

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11-771_2000 200008-0217487
11-771_2000 200008-0217487
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15-771_2000 200008-022064
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Pred. No. 0.03;
0; Mismatches 59; Indels 0;
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Rosen CA, Barash SC, Ruben SM; (HUMA-) HUMAN GENOME SCI INC

NPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

AME/4551 to AME/4702 encode the human immune/hamestopoicatic antigen (I) amino acid sequences given in AME/2710 to AME/3721. (I) have optostatic activity, and can be used in gene therapy and vectine production. (I) proceins and polymoutonoides may be used in the prevention, disponess an treament of diseases associated with imappropriate (I) expression. For example, they may be used to treat disporters associated with decreased expression by rectifying mutations or detailons in a patient's genome Disclosure; SEQ ID NO 28309; 3071pp + Sequence Listing; English.

14-AUG-2000;

ö ther affect the activity of (1) by expressing inactive process or to supplement the patients own production of (1). Additionally, (1) polymotleoxides may be used to production of (1). Additionally, (1) proceeds may be used to produce the serveted (1), by insertling the modific acids into a host cell and culturing the cell to express the procedul. (1) proceins and solvant-forestive may be used to prevent, diagnose and treat immune/haemstopoietic-related diseases, especially additional and an expense the manus immune/haemstopoietic-derived calls. Additional to Addition genomic of Additional the present human immune/haemstopoietic antices genomic of Additional and property and process and control process and control and process and Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds. Gaps Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28310 ö Query Match 15.7%; Score 37.4; DB 22; Length 1576; Best Local Similarity 64.4%; Pref. No. 0.781; Matches 56; Conservative 0; Mismatches 31; Indels 0; Sequence 1576 BP; 407 A; 316 C; 508 G; 345 T; 0 other; 149 CATCCACCTGCCTCTGAGCTTTCACCT 175 795 TGPCCACCTGTCCATCCCATCCACCT 769 AAK73498 standard; DNA; 7954 BP 24-Par. 2000; 0186.54 15-Par. 2000; 0108.50 15-Par. 2000; 00008-0189594 15-Par. 2000; 00008-0189594 18-Par. 2000; 00008-0189594 18-Par. 2000; 00008-01898123 18-Par. 2000; 00008-01898123 18-Par. 2000; 00008-01898123 18-Par. 2000; 00008-01898123 18-Par. 2000; 00008-01898123 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 2000; 00008-01899 11-Tar. 20008-01899 11-Tar. 2000; 00008-01899 2000US-0225266. 2000US-0225267. 2000US-0225268. 2000US-0225268. 2000US-0180628 2000US-0184664 17-JAN-2001; 2001WO-US01354 (first entry) 40200157182-A2 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; Homo sapiens. 06-NOV-2001 09-AUG-2001 AAK73498; AAK73498/c RESULT 888888888888 유 ð à

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AMES4951 to AME64702 encode the human immune/haematopoietic antigen (I) amino acid sequences agiven in Amed2100 to AMMS1701 to AMMS1701 to AMMS1701 to Constitution and asquences agiven in Amed210 to AMMS1701 to Constitution. (I) trace options and activity, and watches and constrained and applymentation of the presentation of the amen and polymentace title and the prevention, dispenses and constrained and polymentace title amen and activity of (I) by expressing inactive procession. For that affects the activity of (I) by expressing inactive process of production of (I). Additionally, (I) that affects and offers and production of (I). Additionally, (I) to apply a control of the affects of the affects of production of (I). Additionally, (I) the ammental of the amental and polymental control of the amental and polymental control of the amental and polymental control of the amental and polymental control of the amental and activity of the amental and activity of the amental and activity of the amental and activity of the amental and activity of the amental activity of the amental and activity of the amental activities of the amental acquence and the present invention. Amental acquence for account and activity of the amental acquences and control invention. Amental acquences and control invention. Amental acquences and control in the amental acquence of the present invention.
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17-NOV-2000; 2000US-0249212.
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05-JAN-2001; 2001US-0259678
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DB 22; Length 7954;

Sequence 7954 BP; 2012 A; 2128 C; 1983 G; 1831 T; 0 other;

Query Match
15.7%; Score 37.4; DB 22;
Best Local Similarity 64.4%; Pred. No. 0.073;
Marches 56; Conservative 0; Mismatches 31;

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11 GTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCCATGTTCAGCAATGTCA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences of the rat sodium channel becape procein, adsignated Alixa94fs. This protein is involved in the generation of pain and other sensory or perceptive nerve impulses, in the establishment and enhance of mod, neurodegenerative and sleep disorders, and in the control of muscle contraction, including movements such as the heartback deligation and vascular cone. The sequences can be used in predictive medicine, sorteening and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New rat sodium channel beta-3 subunit gene isolated from a rat dorsal xoot ganglion cDW library for use in Chromesome mapping, forensic medicine, monitoring olinical trials and therapeutics -
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                                                                                                                                                                                                                                                                                                                  Rat; sodium channel beta3 protein; Alxxa94h5; pain; sleep disorder, neurodegenerative disorder; mood disorder; muscle contraction; ds.
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RK452112 Home appiens FETAL RFLIN Home sapiens CDNA clone CSOPOCATANO 5 - FRINE, mRNA sequence. RK55112114 OF SPETAL RFLIN Home sapiens CDNA clone RK551112 OF SPETAL RFLIN HOME SAPIENS CONTRACTION CLONE CONTRACTION OF SPETAL REPUBLICATION OF SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETAL SPETA
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1. Chassa Lto 97) Princeto Catarini, Hominidae, Homo.

1. Linesa Lto 97) Princeto Catarini, Hominidae, Homo.

1. Linesa Lto Botto Catarini, Hominidae, Homo.

1. Linesa Lto Botto Catarini, Hominidae, Homo.

1. Maybulished Catarini
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AQ8207327
BY730622
AG087943
BH356347
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AQ48173
ALS6488
BX32866
CNSOSCTG
CNSOSM4G
AQ81392
AQ81392
AQ201281
BE181389
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BEZ58128
BZZ68975
CNSOZNIV
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               GenCore version 5.1.6
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Pred, No. 7e-50;
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Matches 215; Conservative
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Bohasidai, Isehara Kanagawa 259-1193, Japan Bohasidai, Isehara Kanagawa 259-1193, Japan Pax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-4505 Fax: 81-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-91-463-9
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HUMSUFY279 Human brain cDNA Homo sapiens cDNA clone NF220-K, mRNA
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// Alone="Grann brain" vector; parkstor" (; ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enrithed chois-extrand cDNA was digested with Not I and closed into the Not I and Econy stees of the pohysboxT (vector library was nor normalized."
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Faraday Avenue Genoscope sequence ID : CS0BAG018ZF03_CS01654_1.
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99.28; Score 236; DB 13;
Best Local Similarity 100.04; Pred. No. 8.2e-56;
Marches 226; Conservative 0; Mismatches 0;
                                                                                                                                                                                    /organism="Homo sapiens"
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/mol_type="mRNA"
                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF023XA09"
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/clone="NF220-K"
/tissue_type="brain"
                                                               Location/Qualifiers
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Oy 185 TAACTCCATCAGACCTCTAGGACCATAAGACTCTGCCAGAACTGAGAGCC 236	z.	_	RPERENCE 1 (bases 1 to 1201) AUTHORS Live. Gruber C., Jessee J., and Polayee, D. TITLE Full-length cDN libraries and normalization JUNEAL Upublisher conscipe cope COMERT Center: demoscope CENTER CENTER CONTROL CONTROL OF STREAMS GENOSCOPE - CENTER NATIONAL de Sequencage B 13, 19, 1906 FWRY cedex - France	Email: seqrefregenescope. Com. 5t. Whe: www.qenoscope.com. fr. Library was constructed by Life Technologies a division of Invitrogen. This sequence belongs to sequence cluster 6147.r For more information about this folluster; see http://www.genoscope.com.fr/ cgi-bi//cluster.cgi?seq-GSODFPC3ANOSOPIscluster=6147.r. Contact : Ferg. html/cluster.cgi?seq-GSODFPC3ANOSOPIscluster=6147.r. Contact : Ferg. html	ACUPTA ANALAGUALININ TERGRATION INVITEDSAN COTPORATION 1800 FEATURES Faraday Avenue Genoscope sequence ID : CSODF023AA05QP1. SOURCE 11201 / Organiam="Homo sapiens"	/mol_type="MRRN" /mol_type="MRRN" /clone="CROBOUSTANO" /tisuue_type="MRRN" BRAIN" /clone_tisuue_type="MRRN" BRAIN" /clone_tisuue_type="MRRN"	/ Inche*Organia braini, Vector; providery; 6, ist etrand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-etrand cDNA was digasted with Not I and closed into the Not I and EoRV sites of the pchyspor court close into the Not I and EoRV sites of the pchyspor court close in the prime and court in the prime and court in the prime and prime	Query Ma Best Loc Matches		DD 1000 ARCAWITGTAITGCATRAGGGGGCGCCCAAAGGG-CCCATCCTTCCTTCATCCTTCCTTCCTTCCTTCCTTCCT	Oy 181 TCCCTAC 188 Db 1119 TCCTAA(1126)	RESULF 6 AKO49286
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VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE

REFERENCE JOURNAL MEDLINE PUBMED

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TITLE

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS

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Ratoh, T. Tacanai, K. Taihai, Y., Itoh, M., Kagawa, I., Kasukawa, T., Ratoh, B., Tacanai, K. Cajinai, Y., Itoh, M., Kagawa, I., Kasukawa, T., Ratoh, B., Kasuka, M., Kadinai, Y., Chinai, M., Ratanai, M., Mahi, K., Momura, K., Mumazak, R., Othoo, M. C., Othoo, M. C., Othoo, M., Sano, H., Sasaki, D., Satai, C., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakai, K., Sakain, M., Direc, Samo, H., Zasaki, D., Satanai, M., Satanai, M., Satanai, M., Sakai, K., Sakain, M., Sano, H., Takahashi, T., Takahai, K., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Takahashi, T., Takahai, A., Sumanishi, A., Takahashi, T., Takahai, A., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., Sakai, M., S
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus; Mus
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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USDA, ABS. US Near Animal Research Center
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Arthropterygili, Metarodom (Dordata, Cramiata; Mereleostomi, Arthropterygili, Meopterygili, Teleosteli, Eureleosteli, Meopterygili, Meopterygili, percomorpus, retraodomtiforenes, Perradomorpus, Petraodomidae, Tetraodom,
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Dass Neto E., Garcia Correa, B., Verjovski.-Almeida, S., Briones, M.R., Goddman, G.H., Carvalho, A.F., Matsukman, A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukman, A., Baila, G.S., Simpon, D.H., Furnetein, A., deOldwalfar, P.S., Buther, P., Osignee, C.Y., O'flare, M.J., Soarce, F., Brentani, R.R., Reis, i.F., de Souza, S.J., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Profise sequence was derived from the PAPESPLICE Human Cancer Genome Profise. This entry can be seen in the following URL (INDER)/Waw.ludwig org bi-feoripps gethemiz.pl?tl=MR3&t2=MR3-GN0229-141100-003-f074E3=2000-11-4&t4=1)
Seq primer: put 18 fc/ward
High quality sequence stear: 51
High quality sequence step: 161.
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Saith, T. B. Abberta, J., Echternkamp, S.B., Chitko-McKown, C.G., Hray, J.B. and Reale, J.M.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished
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Boyldae; Boylinae; Bos.
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Laboratory of Cancer Cancer Research
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Best Local Similarity 64.3%; Pred. No. 0.24;
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Matches 63; Conservative 0; Mismatches 35; Indels
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CHE20-193A19: TU CHOR1-230 Segment I Rattus norvegicus genomic clone
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A., Gebregeorgia, E., Overton, L., Russell, D., Chen, D., Rigga, F., de
Rong, P. and Freser, C. Verton, L., Russell, D., Chen, D., Rigga, F., de
Rong, B., G. M. Geguence from Library CHORI-120 Econit segment
       Submitted (112-ARP_2000) Genegosope - Centre National de Sequencage : Bp. 1910 65 TWY cedex - FRANCE (E-mail : sequefagenoscope.cnn.fr. - N8b : Www.genoscope.cnn.fr. - N8b : Www.genoscope.cnn.fr. - Sequefagenoscope.cnn.fr. - Sequefagenos
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Mammalia, Eutheria, Rodentia, Sciurognachi, Muridae, Muxinae,
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/mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
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Pred. No. 1.2;
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- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
This sequence is a single read and was generated as part of a large
genome. For more Information, please take a look at
http://www.genoscope.cns.fr/getraddon.
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ALL14370. 1G1787189
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Tetracdon nigroxizidis
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/clone_"Genoscope sequence ID : COAGZ60BD03LF1-end : T7"
/note="Genoscope sequence ID : COAGZ60BD03LF1-end : T7"
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                                                                                                                                                                                                                                                                                                                                        /oxganism="Tetraodon nigroviridis"
/mol type="genomic DNA"
/db_xref="taxon:99883"
/clone="260606"
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Dikaryofa; Wetaroa; Chordera; Cranista; Vertebrata; Euteleostomi; Menaroa; Cranista; Framaces; Ctearrhini; Hominidae; Inono.

In Manaroa; Lot 678)

Wahairas (3.6. Maillaco, J.C., Smith, K., Swartell), S., Holzman, T., Mahairas, Liaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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/clone_lib="CHOR1-230 Segment 1"
/note="Vector: pTNRRAKC2.1; Site_1: EcoR1; Site_2: EcoR1;
-CHOR1-230 Rat (SN/SsMed/McN) ENC library produced by
Fater de Jong*
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High Throughput Sequencing Center
University of Meashington
University of Meashington
1401 Queen Anne Avenne North, Seattle, WA 98109, USA
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/focte="Organ: sperm; Vector: pBcloBACil; BAC Clones in
E-Coll HH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
9938080
                                                                                                                                                                                                                                                                                                                                                   16.8%; Score 40; DB 28; Length 611; 58.3%; Pred, No. 1.2; tive 0; Mismatches 50; Indels
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/mol_trype="genomic DNA"
/db_xref="taxon:9608"
/clone="Platce=3173 Col=16 Row=p"
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Location/Qualifiers
/clone="CH230-193A19"
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                                      /sex="Female"
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Homo sapiens
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Score 39.2; DB 28; Length 676; Pred. No. 2;

16.5%;

Query Match Best Local Similarity

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/Ab.longe.To Coll strain XID-Good Tr-sentent, P-*
/Ab.longe.To Coll strain XID-Good Tr-sentent, P-*
/Alone libe-Wouse lobe pleaned wucklib library
/Ances Teacher Pholozy: Partified genomic DNA from M.
musculus GS78L/63 (male) was obtained from the Jackson
Laboratory Wouse DNA Recourse charing the Jackson
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by respected passage through a
0.005 lnoh oritice at content valocity. The sheared NNA
pass hunt end-reputed with 70 DNA polymerses and 74
playmed or the Kinnes Adaptor olisomicleotides were
adaptored DNA was purified an Agia-male exceeds The
adaptored DNA was purified an Agia-male exceed SP 10.
10.5 Dr range using preparative agarose ged for a 3.5 to
electrophoresis. Vector DNA was prepared from a derivative
for DNDA2 (gil 473214) [gb] AR129073.11, a copy-number
inductale derivative of planning R1. The vector was ligated
with adaptore complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
adaptored vector DNA, and transformed into
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LM0469M04F Wouse 10kb plasmid UUGCIM library was musculus genomic
clone UUGCIM0469M04 F, genomic survey sequence.
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Ilmert Length.2000 Std Error: 0.00
Plate: 0469 Town W. column: 0477000 Seq primer: 0477070AAACGACGACCAGT
Class: plasmid ends
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/strain="C57BL/6J"
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/clone="UUGC1M0469M04"
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Normalization and subtraction of opt-trapper-salected cDNs to prepare full-langth to MN libraries for rapid discovery of new genes Genome Rea. 10 (10), 4617-4530 (2000)

RIESM integrated sequence analysis (RISA) system-384-format sequencing pipeline with Stone Maniticapillary sequence. Genome Res. 10 (11), 757-1717 (2000)

Computer-based methods for the mouse full-langth cDNA encyclopedia real-time sequence Clustering of Construction of a nonrectundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CMN library was prepared and sequenced in Mouse Genome Res. Construction of a nonrectundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

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                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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UR.hittp://genome.gen.riken.go.jp,
dadochi,J., Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashinume, H., Haybshida,K., Hirconan,T., Hori,F., Imoteni,K.,
Elbhi,Y., Icoh,M., Kagawa,J., Koyia,Y., Kondo,S., Konno,B., Kondo,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K.,
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Scale : Innee end sequencing project of the Terracdon nigrovizidis genome. For more information, please the come information, please can en en EFF trackedon.

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                                                                                                                                                   Rosst Crollius, H., Jaillon, O., Dasilva, C., Bonneau, L., Fisher, C., Bernt, A., Fisher, C., Mincker, P., Brottier, P., Quetier, F., Saurin, W. and Weitsenboth, J. Estimate of human gene number provided by genome-wide analysis using Tetrackon nigrovitidis DRA sequence
Net. Genet. 25 (2), 235-238 (2000)
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ALIGNMENTS

Published Applications Man. Man. 1897 PUBCOMB. seq. 1
21. GGPZ 6 (Publications Man. 1897) PUBCOMB. seq. 1
22. GGPZ 6 (Publication) FURN PUBCOMB. seq. 1
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Sequence 4, Application US/09997579 Patent No. US20020113203A1 SEQ ID NO 4 LENGTH: 1261 US-09-997-579-4

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TYPE: DNA ORGANISM: Homo sapiens

US-09-997-579-4

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CURRENT TRILICATION UNDERSE: U8/00/-01-17
PRIOR APPLICATION DATE: COD.-01-17
PRIOR APPLICATION TO THE WASHER OF SEQ ID NOS: 10231
SOFTWARE PREENTIN Ver. 2.0
LENGTH: 4625
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Publication No. US200300780841
SMREMA, INVORMATION:
APPLICATE, Rosen et al.
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CORGANISM: Homo sapiens
US-09-764-891-7659
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US-10-034-650-55
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Best Local Similarity
Matches 68; Conserv
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105 CTTCCCTTCATGCATCCTTCTTCTTCATTCATCCATACATCCACCTGCCTCTG 164
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Sequence 25531, Application US/10027632

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PRICAR PLACATION WINGERS: US 60/218,006
PRICAR PLACATION AND SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURCE OF SOURC
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SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 57; Conserv
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; ORGANISM: Human
US-10-027-632-215913
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LENGTH: 1327
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GENERAL PROPAGRAPH OF USE OF OTHER PROPAGRAPH OF TITLE OF INVESTORS INCLOSED OF OTHER PROPAGRAPH OF TITLE OF INVESTORS I TO SOLVE TO SOLVE THE REPRENCE I 109827.1.29 CURRENT PROPICATION NUMBER OF 120020.

CHESTER REPRENCE: 109827.1.29 CURRENT FILING DATE: 2002-04-50
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                                                                                                                                                                                                                 Query Match 15.9%; Score 37.8; DB 12; Length 1091; Beet Local Similarity 64.0%; Pared. No. 0.025; Beet Local S7; Conservative 0; Mismatches 33; Indels 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Sequence 30772, Application US/10027632
; GENERAL INFORMATION:
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        ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-30772
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SOFTWARE: FABLESE
SEQ ID NO 30772
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Sequence 718:04.04. Own Proprietion UB/09954531.

GERREAL INFORMATION: PROPRIATION: 2000-09-20 (20/234,09)

PRIOR PRILICATION INVEST: US/06/234,09

PRIOR PRILICATION INVEST: US/06/234,59

PRIOR PLILING DATE: 2000-09-20

PRIOR PLILING DATE: 2000-09-20

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APPLICANT: Kulgard, Rollert H.
APPLICANT: Getraduck Enkeh
APPLICANT: Getraduck Enkeh
APPLICANT: Getraduck Mobert H.
APPLICANT: Yamanou Lawo.
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                                                      Score 37.8; DB 10; Length 3768;
Pred. No. 0.039;
0; Mismatches 42; Indels 0;
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Pred. No. 0.039;
0; Mismatches 42; Indels 0;
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                                                               Query Match
Best Local Similarity 60.0%;
Matches 63; Conservative
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SOFTWARE: Patentin version 3.0
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ORGANISM: Homo sapiens
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Bert Local Similarity 60.0%; Pred. No. 0.039;
Matches 63; Conservative 0; Mismatches 42; Indels 0;
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Patent No. US20020102532A1
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Patent No. US20020165180A1
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SEQ ID NO 164
LENGTH: 3768
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GORGANISM: Homo sapiens
US-09-954-531-164
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US-09-969-708-464
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Sequence 20093, Application US/10027632
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GENERAL INFORMATION (US2003020478A9
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TITLE OF INVENTION: Deliveration and Mapping of Single Nucleotide
TITLE DE INVENTION: Polymorphisms in the Human Genome
FILE REPRESENCE: 108273, 129
CHERRY APPLICATION NUMBER: 105/10/027, 632
CHERRY APPLICATION NUMBER: 105/02/021, 632
CHERRY APPLICATION NUMBER: 105/02/021, 632
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US-09-873-119-689
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US-09-960-706-1041
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0; Mismatches 42; Indels
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Matches 63; Conservative
                                                   SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 689
LENGTH: 3768
                 NUMBER OF SEQ ID NOS: 755
                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Title:
US-09-936-680-4
Perfect score: 126;
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Scoring table: OLIGO NUC Gapop 60.0 , Gapext 60.0

Searched: 2888711 seqs, 20454813386 residues

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Pred. No. is the number of results predicted by chance to have a

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beta 3:7. an additional auxiliary subunit of the voltage-sensitive sedium channel that modulates channel gating with distinct kinetics Proc. Natl. Acad. Sci. U.S.A. 97 (5), 2308-2313 (2000)
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Pinnock, R.D., Highes, J., Richardson, P.J., Mizuguchi, K. and
Jackson, A.P.
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WARNER LAMBERT COMPANY (US) ; Cambridge University Technical
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                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
366 c 372 g 26
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1201 GACTCCCTAACTCCATCAGACCTCTACGACCATAAGACTCTAGGACCGC 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AAGCTGGAGTTCCGGGGTGGGCGGAGGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCGGCCCGGAGCGGCTGATCGCTCCCTCGAACTCGGGAGGTCCAGTGGGGGTCGCTTAG 180
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                                                                                                                         function="modulates channel gating kinetics"
                                                                                                                                                                                  /evidence=experimental
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/gene="scn3b"
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Best Local Similarity 100.0%;
Matches 1261; Conservative 0
                                     /gene="scn3b"
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Best Local Similarity
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                                                                                                                                                                                                                                                      843 GGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATCGT 902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryoča, Metazoa, Chordata, Craniata, Vertebxata, Buteleostomi,
Mammalia, Butheria, Primates, Cataxrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1203 CICCCIAACTCCATCAGACCICTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1631 CTCCCTAACTCCATCAGACCTCTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1687
723 CCTCTACACCTGCAATGCTCCCGGGGGTTTGACTTTGAGTCGCCATCGGCCCTTTGTGAA
                                                                                                                             783 GACGACGCGCCTGATCCCCCTAAGAGTCACCGAGGAGGCTGGAGGACTTCACCTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5306 bp mRNA linear F
AB032984, STAA1158 protein, partial ods.
AB032984.1 GI:6330135
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/clone_lib="pBluescript11 SK plus"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="hj00081"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                551 GGGCGCGGAGCGGCTGATCAGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAGGG 610
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/note="Start codon is not identified."
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1129 TICCCITCANGCANCCATHGINCIGINCATHCATHCATHCCANCCACCHGCCTCTGA 1188
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Chemistry Dve-terminator Mramesham; 100% of reads
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Chemistry Dve-terminator Mramesham; 100% of reads
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Chemistry 120% bases at least QAO
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Name, Control of Assas, C., Adio Oddola B., All-Josman, F.R., Allen, C., Adio Oddola B., All-Josman, F.R., Allen, C., Adio Oddola B., All-Josman, F.R., Allen, C., Adio Oddola B., All-Josman, F.R., Allen, C., Banker, C., Brief, R. C., All-Romarten, C., Brief, R. C., All-Romarten, C., Brief, R. C., Carton, R. C., Coyle, M. B., Brief, R. C., Carton, T. Carter, M. Cavazos, S.R., Checko, J., Chavazo, D., Carton, M. Carton, C., Coyle, M. D., Dathorne, S.R., David, R., David, C., David, C., David, C., David, C., Carton, M. Cavazos, S.R., Checko, J., Chavazo, D., Carton, C., Coyle, M. D., Dathorne, S.R., David, R., David, C., David, R., David, C., Coyle, M. D., Dathorne, S.R., David, R., David, C., Coyle, M. D., Dathorne, S.R., David, R., M. Palla, M., Carton, C., Coyle, M. D., Dathorne, S.R., Mariton, K., Balland, C. D., Cox, C., Coyle, M. D., Dathorne, S.R., Haniton, K., Balland, C. D., Cox, C., Coyle, M. D., Dathorne, S.R., Haniton, K., Balland, C. D., Cox, C., M., Carton, C., Coyle, M., David, C., Mariton, K., Marris, K., Hatt, M., Halle, R., Halle, S., Haniton, K., Balla, A., Gorrell, J. H., Odevara, M., Gunzathe, P., Hale, S., Haniton, K., Hernandez, O., Hodgoon, A., Hognes, M., Kord, J., Foerer, P., France, C., Hodgoon, M., Hognes, M., Wollins, B., Carton, M., Carton, M., Carton, C., Halle, M., Martinez, E., Marris, K., Hatt, M., Halle, S., Warting, S., Gorden, M., Martinez, E., Martin, C., Hall, J., Halle, S., Marting, S., Martin, R., Marting, S., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C., Martin, C.
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28772 CCAGCCCAAAAATGCTTGCTTCAATAATTGTTTCCCCTGGCTTCTCGTGGTTAT 28733
                                                                                                                                                    28832 AGAATCTGAGAGGGGGGAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAAGCCG 28773
                                   28892 CCTTCCTTCGTCAGAAAGTCGCCCCTGGGGGCAGTTCGTCCAAAGGGTTTCCTCGAA 28833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACUSS921 144833 bp DNA linear HTG 08-JAN-2003
HOmo sapiens chromosome 3 clone RP11-142P10, WORKING DRAFT
SEGUENCE, 13 unordered pieces.
                                                                                         303 AGAATCTGAGAGGGGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAAGCCG 362
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Homo sapiens (human)
Homo sapiens
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2 (bases 1 to 144833)
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Direct Submission
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121144. ,125917
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NOTE: This is a "working draft, sequence. It currently consists of 8 contigs. The true order of the pieces is not known and theirs roder in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Maps between the contigs are represented as arbitrary. Must be exact sizes of the gaps are unknown. This record will be updated with the finished eagement as soon as it is available and the accession number will be preserved.
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100.0%; Pred. No. 1.2e-233;
ive 0; Mismatches 0; Indels 0;
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126018. .127347
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/db_xref="taxon:9606"
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Homo saptora chromosome 11 clone RP11-11C15 map 11, WORKING DRAFT
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Mammalia; Butheria; Primates; Cararrhini; Hominidae; Homo.
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                                                                                                                                                             183 CCCABAGCCCCACCCGGCTCCBAAGCTCCCAGGGCCTCCCCAGGCACCGGTGCTCGGC
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                               Query Match

33.9%; Score 428; DB 2; Le Best Local Similarity 10.0%; Pred. No. 1.2e-233; Matches 428; Conservative 0; Mismatches 0;
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Homo sapiens (human)
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(see http://www.hget.bm.fmc.edu/doc/denbank_draft_data.html).
MOTE This is a "working that" sequence. It currently
consists of it of courtyer. The true order of the pieces
is not known and their order in this sequence record is
Submitted (22-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (Dasse 1 to 144833)
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Chemistry. Dye-reminator Big ope: 86t of reads
Chemistry. Dye-reminator Big ope: 86t of reads
Consembly program: Phrapy version, 099339
Consembly program: Phrapy version, 099339
Consembly program: 27260 bases at least 090
Consembly quality, 132735 bases at least 030
Consembly quality, 135139 bases at least 030
Consembly description of 13510795; such of contige setimation quality coverage: 4x in 020 bases; sum-of-contigg setimation quality coverage: 4x in 020 bases; sum-of-contigg setimation
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43818. qsp of unknown length
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111857: contig of 28448 bp in length
111957: gap of unknown length
144833: contig of 32876 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: HAXY
Center clone name: RP11-142P10
Center clone name: SP11-142P10
Sequencing vector: M13;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                             Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                        Center: Genome Therapeutics Corperation
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(bases 1 to 172546)
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                                                     Smith, D.R.
                                             AUTHORS
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Pred. No. 1.2e-233;
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87948. .97279
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114307. .129830
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106138. .114206
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Debriced (NoT-2000) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, NA 70453, USA
Street, Waltham, NA 70453, USA
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  (e.mail.hattoriages.c.itken.go.jp, URuhttp://hgp.gec.riken.go.jp/,
Tels-14-503-911, Faxsal-45-503-910,
On Nov 5, 2001 this sequence version replaced gi:12381934.
Location(Dualifiers
                                                                                                                                                                                                                                                                                                              Bokaryofa, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi; Momanii, Butheria, Primates, Catarrhini, Mominidae, Homo.

(Mameali, Entheria, Primates, Catarrhini, Mominidae, Homo.

(Maneali, Entheria, Primates, Catarrhini, Mominidae, Homo.

(Banchi, Primates)

(Genome Therapeutics Corporation Sequencing Center: Human Genome
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from Sapiens chromosome 10 clone RPI1-321E15, complete sequence.
ACG69539
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Pred. No. 1.2e-233;
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                                                                                                                                                       /map="11g"
/clone="RP11-634B22"
46062 a 39655 c 41140 g 51312
                                                                   1. .178169
/organism="Homo sapiens"
/organism="Homo sapiens"
/oll_type="genomic DNn"
/db_xref="taxon:9606"
/chromosome="11"
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2 (bases 1 to 181471)
Smith, D.R.
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Homo sapiens genomic DNA, chromosome llq clone:RP11-634822,
complete sequence.
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172546: contig of 37128 bp in length.
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Best Local Similarity 100.0
Matches 428; Conservative
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AP002749 170411 bp DNA linear H7G 13-JUL-2000 Mone sapiens chroneseme il clone RP11-158021 map l1q24, WORKING DNAFF SEQUENC, 41 unordered pleces.
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1 (Dase 1 to 1784) Imates Catarthin; Homitidas Homo.

Prijsymas, Vada, T. Toyoda, A. Taylor, T.D., Hong-Seeg, P. Prijsymas, A. Yada, T. Toyoda, A. Metanabe, H. and Sakai, Y. Published Only in DateBase (2000)

Published Ito 178431

Hattori, M. Idhii, K. Toyoda, A. Taylor, T.D., Hong-Seeg, P. Hattori, M. Idhii, K. Toyoda, A. Taylor, T. Dilor, M. Manabe, H. and Sakaki, Y. Dilor, M. Manission

Direct Submission
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199 ACGGIGGIGGAAIGGIICIACIACAGGCCCGAGGCGGIAAGAITICCIIAITIACAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 CGGAATGGCCACCAGGAGGGGGGGGAGAGCCCCTTTCAGGGGGGCGCCTGCAGTGGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 471;
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100.0%; Pred. No. 6.9e-174;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                               /organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
126 c 143 g 1
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HTG; HTGS PHASE1; HTGS DRAFT.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 324; Conservative
                                                                                                                                                            DAVID MERBERG,
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         Smith, Date t submission
Submitted (19-07-2000) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
4 (bases 1 to 181471)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGCGCGCAGCGGCTGATCGGCTCCCTCGAACTGGGGAGGTCCAGTGGGGTCGCTTAGGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CCCAAAGCCCCCACCCGGCTCCAAAAGCTCCCAGGGCCTCCCCAGGCACCGGTCCTCGGC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 CCTTCCTTCGGTCAGAAAGTCGCCCCCTGGGGGCAGTTCGTCCCAAAGGGTTTCCTCGAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 AGAATCTGAGAGGGGGCAGTCCTTGACCGAGGGAATCTCTCTGTGTAGCCTTGGAAGCCG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 CCAGCCCCAGAAGAIGCCIGCCTICAATAGAITGTTTCCCCCTGGCTTCTCTCGGGCTTAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Stropcophyta, Embryophyta, Tracheophyta;
Sprantophyta, Hagnoliophyta; Lilopsida, Poales, Poaceae, BACCAD
Slade, Panicoldaes, Andropsomees, Zea.
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Jacobs, K., Mccoy J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
Treacy, M., Spaulding, V. and Agostino, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                        33.9%; Score 428; DB 9; Length 181471;
100.0%; Pred. No. 1.2e-233;
tive 0; Mismatches 0; Indels 0;
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Matches 428; Conservative
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MOTE: This is a "working draft, sequence, it currently consists of chorids. The concides the true order of the piaces is not known and their order in this sequence record is arbitrary, daps between the corder in this sequence record is arbitrary, daps between the corder in this sequence around in the the chart sizes of the gaps are unknown. This second will be updated with the failshed sequence are unknown. This second will be updated with the failshed sequence secon as it is available and the accession number will be 12012 hn in lengt! preserved

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 | 4644 | 1953 | 5215 | 5562 | 5833 | 2020
 | 5234 | 5480 | 6703 | 5916 | 7105 | 7293 | 7418
 | 7572 | 7690 |
| 311 | 477 | 474 | 329 | 022 | 782 | 471 | 110 | 628 | 368 | 061 | 9559 | 0236
 | 0596 | 1124 | 1602 | 2184 | 2563 | 2802
 | 3128 | 3282 | 3566 | 3810 | 4129
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^{1/2804 //8912} contig of 1076 bp int length 1/7006 178431 contig of 1426 bp int length.

* NOTE: This is a "working draft" sequence. It currently e consists of 41 contigs. The true order of the pieces is not known and their order in this sequence record is

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Homo eaplena chromosome Chromosome 10 cione RP11-331019, WORKING
DRAFT SEQUENCE, 22 unordered pieces.
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SUMMARIES

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ALIGNMENTS

Bukaryotsa Metasoa, Chordata, Craniata, Vertebrata, Euteleostomi, Memmalia, Eutheria, Primates, Catarrinii, Meminidae, Homo.

1. Chaso and Leo 1201, Jessee, J. and Polayes, D. Lil, M. M. Colbert, C., Jessee, J. and Polayes, D. Pull.-i, Grapti Golba, Libraties and normalization REFERENCE AUTHORS TITLE JOURNAL COMMENT

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                                                                                                                                                                                                                                                                                                           Bikarycisi Metazon: Chordeta: Craniates i Vertebrates Buteleostcomi;
Memmalia, Buthberia; Prinstess; Cataritini, Hominidae; Homo.
1. (Cheses 1 to 130) Prinstess; Cataritini, Hominidae; Homo.
Is, W.B., Gruber, C., Jessee, J. and Polayce, D.
Pall-Langth CDRA, Librasies and normalization
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myor information about this cluster, see
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capi.bhrp.//cluster.cgifseq-cgiArb00622809146Juster=ei147.r. Contact
Feng Midsi Bmall. Filangshifsetech.com VBL :
Freng Midsi Bmall. Hivhtrogen.com/ Illytrogen Corporation 1600
Faradey Avenue Genosope Sequence ID : CS1AF00628050P1.
Location/Qualifetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 GAGGAGGTGGAGGCCACCACGGTGGTGGTTCTACAGGCCCGAGGGCGGTAAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |organism="Homo sapiens"
|mol_type="mRNA"
|db_xref="taxon:9606"
|clone="CSODF023YA09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAACGACTCTGGCCTCTACACC 732
                                                                                                                                                                 BX445002.1 GI:30782286
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Matches 384, Conservative
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                               /Clore_lib_widow sapiess FFPAL BRANNW
/Anote-Togram brain Vector; pGWNSOQFF 6: 1st strand CDNA
/Anote-Togram brain Vector; pGWNSOQFF 6: 1st strand cDNA
was primed with a Nocl-oilgo (GP) primer Five prime end
enriched, cobble-errand cDNA was digested with Noc I and
cloned into the Noc I and EcoRV aits of the pGMVSEDRF 6
vector. Library was non nonmalized.*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGCCCTTTGTGAAGACGACGCGGCTGATCCCCCTAAGAGTCACCGAGGAGGTTGGAGAG 828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      805 TGGCTGCTCATCGAGATGATATATTGCTACAGAAAGGTCTCAAAAGCCGAAGAGGCAGCC 864
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624
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           Faraday Avenue Genoscope sequence ID ; CSODF023AA05QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.6%; Score 600; DB 13; Length 1201; 99.7%; Pred. No. 1e-278; Live 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1009 CCAGTGGAGGAATAGAACAGGAGCAGTGTGACATGAGGTGGC 1050
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                                                                                                                                                                                                                                                                             /tissue_type="FETAL BRAIN"
/dev_stage="fetal"
                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF023YA09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.7
Matches 700; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      694
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1. (Dases 1 to 1069)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 6.8e-128;
306 TCCATCAGACCTCTAGGGACCATAAGACTCTGGCAGAACTGAGAAGCC 353
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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BP 191 91006 ENVE voetex - Francee he : www.genoecope.cna.fr
Bmall: seque@egenoecope.cna.fr Neb : www.genoecope.cna.fr
Linkrary was constructed by Life Technologies, a division of
Invitrogen. This sequence blongs to exquence cluster 6447.r For
more information about this cluster, see
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contact: Peng Likang Bmail. filangalifetedn.com UKL:
Contact: Peng Likang Bmail. filangalifetedn.com UKL:
http://tullangth.invitrogen.com/ InVitrogen coporation 1600
Paxaday Avenue Genoscope sequence ID : CSOBAGO18ZF03_CSO1654_1.
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11.W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization
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/mol type="mRNA"
/db xref="taxon:9606"
                 615 CTGAACGACTCTGGCCTCTACACC 638
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HUMSUPY279 Human brain CDNA Homo sapiens CDNA clone NF220-K, mRNA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Ikeda, J.
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/clone lib="Human brain cDNA"
130 c 82 g 120 t
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Matches 215; Conservative 0; Mismatches
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Email: shinji@nga.med.u-tokai.ac.jp.
Location/Qualifiers
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/clone="NF220-K"
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'Alore argogan: herally Vector: pow/MSPORT, 6, lat strand cDNA
'Actors"Organ: herally Vector: pow/MSPORT, 6, lat strand cDNA
was primed with a Norl-Oilgo(dT) primer. Five prime end
enrighted, double-errand cDNA was digented with Not I and
cloned into the Not I and ScoRV sites of the poWNSPORT 6
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vector. Library was not normalized.
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Fig. 191 91006 EVRY cedex - France
Email: sequescopencecope..nu Eff. Web : www.genoecope.cns.fr
Library was constructed by Life Tochnologies, a division of
Invitrogen This sequence belongs to dequence cluster 6147.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ogsi-bin/Cluster.cgi?deg-cSoDFOOSBOIQFlacluster.e6147.r. Contact
Forgo Lida Call : filiangel/fletech.com/RL:
http://fulllangth.invitrogen.com/Invitroden Corporation 1600
Faraday Avena Gensecope agenence ID : CSODFOOSBOIQFI.
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ALS34136 Homo sapiens FETAL BRAIN Homo sapiens CDNA Clone
CSDDF00CSY102 5-PRIME, MRNA sequence.
Score 268; DB 9; Length 1201;
Pred. No. 3.2e-118;
0; Mismatches 0; Indels 1
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/mol_type="mRNN"
/db_xref="taxon:9606"
/clone="CSODEO05Y102"
/tissue_type="PETAL BRAIN"
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//Clobe 101-WILL MOSTIL WECKTE, Site 1: Not1;
//Clobe 101-WILL MOSTIL WECKTE, DCWY-SPORTE, Site 1: Not1;
Site 2: RockW (destroyed): RNA source anonymous pool of 6
male brains as errong 2.3.7 yo. Libhary is olido-dr
primed and directionally cloned (BookW site is destroyed upon cloning). Average insere size 1.5 Rb, insert size tange 1.3 Rb. Libhary is normalized and enriched for full-length Colones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 0.19. Note: 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 a MHP MOSC Library 18 normalized and enriched for 18 and 18 normalized and enriched for 18 normalized and enriched for 18 normalized and enriched for 18 normalized and enriched for 18 normalized and enriched for 18 normalized and enriched for 18 normalized and enriched for 18 normalized and enriched for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized for 18 normalized
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (Roses I to 926)
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1. (Dases: Leo 972)
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Tissue Procurement Life Technologies, Inc.
OMN Library Preparation Life Technologies, Inc.
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National Institutes of Health, Mammalian Gene Collection (WGC)
Unbublished
Contact: Robert Strausberg, Ph.D.
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8.6%; Score 109; DB 13; Length 972;
Best Local Similarity 99.4%; Pred. Ro. 2.28-41;
Matches 159; Conservative 0; Wismatches 1; Indels C
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5762608"
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BQ066875.1 GI:19895921
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Site 2 Excpw (destroyed) RNA select enonymous pool of 3 Site 2 Excpw (destroyed) RNA select enonymous pool of 3 Site 2 Excpw (destroyed) RNA select enonymous pool of 3 dark male age 2 weeks. Library is oligo-dT printed and directionally cloned (Except site 2) the library is oligo-dT printed and clineding). Aregage insert site 1.7 Nb. insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: 5 a 187 g as a NH MECLibrary 10.
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Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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12.2%; Score 154; DB 13; Length 509;
Best Local Similarity 100.0%; Pred. No. 3.5e-65.
Matches 154; Conservative 0, Mismatches 0; Indels 0
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/lab host="DH10B"
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/db_xref="taxon:9606"
IMAGE:5769987, mRNA sequence.
BX280396
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                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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ANGNATIC:NRHY4-00042-H5-A W Rat hypothalamus (10464) Rattus norvegicus CDNA clone nrhy4-00042-h5 5', mENA sequence. CE730533. G17:29797666
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Messo, Locaria, Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, M. Ur., Zago, M. M., Dordin, S., Costa, F. P.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            /clone_lib="W Rat pituitary (10477)"
fore="Vector: pSPORTI, Site 1: Sall; Site 2: Notl; W
fututary adult female Wistar rat avg insert size 2.1
10.10.10.29.93 t 55 others
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Similarity 100.0%; Pred. No. 4.2e-07;
18; Conservative 0; Mismatches 0;
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1 Similarity 100.0%; Pred. No. 4.2e-07;
38; Conservative 0; Mismatches 0;
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1. .472
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Amgen EST Program.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Pate: 8014 47-4881
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/db_xref="taxon:10116"
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UI-M-BH3-beq-d-04-0-UI 5', mENR sequence.
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                         /organism="Rattus norvegicus"
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Seq primer: puc 18 forward 1914) High quality sequence exert: 19
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Location/Qualitiers
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Goldman, G.H., Carvalho, A.F., Mateukuma, A., Baia, G.S., Simpson, D.H., Brunscein, A., Geoliveirar, P., Suncher, P., Jongeneel, C. Y., O'Hare M.J., Serges, F., Brentani, R.R., Peis, L.F., de Souza, S.J. and
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                      Laboratory of Cancer Genetics
Manya Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                               Shofgun sequencing of the human transcriptome with ORP expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Pate: 8061 37-4881
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100.0%; Pred. No. 3e-05;
ive 0; Mismatches 0; Indels
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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="bkult"
/clone_lib="TT0002"
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Rattus norvegicus
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Amgen, Inc
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Query Match 2.3%; Score 29; DB 12; Length 636; Best Local Similarity 10.0%; Pred. No. 0.01; Macches 29; Conservative 0; Mismatches 0; Indels Macches 29; Conservative 0; Mismatches 10; Indels 610 AATGGCCACCAGGAGGTGGAGAGCCCCTT 638 241 AATGGCCACCAGGAGGTGGAGAGCCCCTT 269

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Published Applications Mix; 1) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 2) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 3) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 3) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 5) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 5) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 6) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 6) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 9) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 10) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 11) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 12) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 13) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 14) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 15) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 16) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 17) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 18) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 19) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 10) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 11) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 12) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 13) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 14) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 15) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 16) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 17) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 18) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 19) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 10) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 11) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 12) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 13) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 14) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 15) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 16) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 17) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 18) (1907 6/ptodate // Jubpan / USO PubCOMB. seq; * 19) (1907 6/
Database

Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		SUMMARIES		
Query Match Lengt	BO d	13	Description	
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.0	5 13	US-10-029-191-21	Sequence 21, Appl	
.0 222	0 10	US-09-997-579-3	Sequence 3, Appli	
.0 263	2 13	US-10-029-191-22	Sequence 22, Appl	
.0 310	13	US-10-029-191-1	Sequence 1, Appli	
.6 57	11 11	US-09-764-891-1293	Sequence 1293, Ap	
6.	14 12	US-10-121-759-20	Sequence 20, Appl	
	12	US-10-121-759-19	Sequence 19, Appl	
	6 23	US-09-864-761-15643	Sequence 15643, A	
	11 12	US-10-027-632-132914	Sequence 132914,	
	11 13	US-10-027-632-132914	Sequence 132914,	
	7 10	US-09-712-363-4		
	14 14	US-10-219-219-3	Sequence 3, Appli	
	2 9	US-09-864-761-679	Sequence 679, App	
	12	US-10-027-632-86250	Sequence 86250, A	
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Query Match Best Local Sim: Matches 1261;	Quary Match 1261; Score 1261; DB 10; Length 1261; Sest Local Sfmilarity 100.04; Pred, No. 0; Matches 1261; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QX DD	1 CCCTCCCTTCCGAGCTTAACCTTACCCTGAGCGAGCGAGC
% 9a	61 AAGTROGAGTROCCOGGAAGCAACTCCCTGCTGCTGCGCGAGCCGCGAGA 120
è 6	121 acasacacacacacacacacacacacacacacacacaca

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1044 AGGIGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCAG 1103
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UG-10-029-191-21

Sequence 21, Application US/10029191

Sequence 21, Application US/10029191

GREEBAL IMPORATION: ROLY A.J.

TITLE OF INVENTION: ROLY A.J.

TITLE OF INVENTION: ROCKASU,

TITLE OF INVENTION: ROCKASU,

CURRENT PRILICATION NUMBER: US/10/029,191

CURRENT PRILICATION NUMBER: US/10/029,191

CURRENT PLICATION NUMBER: 09/569,978

PRIOR PLILING DATE: 2000-05-12

PRIOR PLILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 23

SOFTWARE ROCK SEQ ID NOS: 23

SOFTWARE ABERTON NOS: 23

LEMBATH: 64
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ilarity 100.0%; Pred. No. 7.5e-10;
Conservative 0; Mismatches 0; Indels
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                 361 COCCAGCCCCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTT 420
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APPLICANT: GITHIS, ROYA, A.J.
TITLE OF INVENTION: ROYAL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBDNIT
TITLE OF INVENTION: PROFESTI
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FRIOR RELINGTON INVENTE: 09/569,979
FRIOR APPLICATION NUMBER: 09/569,979
FRIOR APPLICATION NUMBER: 09/514,196
FRIOR PELING DAFF: 1999-06-14
SOGFWARE: RELING DAFF: 1999-06-14
SOGFWARE: RELING DAFF: 1999-06-14
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LEMONTHER OF SECULD NOS: 21
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Publication No. UBS0000077808A1
Publication No. UBS0000077808A1
Publication No. UBS0000077808A1
APPLICATION: None or a.1.
TILLE OF INTERFERENCE: PCOOG
CURRENT PRINCE PYETS: 2001-01-17
CURRENT PRINCE PYETS: 2001-01-17
CURRENT APPLICATION NUMBER: UB/097764, 891
CURRENT APPLICATION NUMBER: UB/09764, 891
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100.0%; Pred. No. 6.9e-10;
iive 0; Mismatches 0; Indels (
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
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OTHER INFORMATION: n equals a,t,g, or c
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-1293
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OTHEN INCOMPATION: n equals a,t,g, or
NAME/KEY: SITE
LOCATION: (556)
OTHEN INPOMPATION: n equals a,t,g, or
NAME/KEY: SITE
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Best Local Similarity 100.0
Matches 38; Conservative
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ORGANISM: Homo sapiens
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CORGANISM: Rattus sp.
US-10-029-191-1
                                    GENERAL INFORMATION:
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| Publication No. 1023002100453A1
| GEREAL INFORMATION: OUTCOLOGISTAL
| APPLICATION NO. 1023002100453A1
| APPLICANT CURTIS, ROYA A.J.
| TITLE OF INVENTION: PROTEIN
| FITTE OF INVENTION: PROTEIN
| FITTE PRESENCE: 21014.0.0007/501
| FITTE PRESENCE: 21014.0.0007/501
| FITTE OF INVENTION: PROTEIN
| FITTE PRESENCE: 21014.0.0007/501
| FITTE OF INVENTION: PROTEIN
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| FITTE OF INVENTION: PROTEIN
| FITTE OF INVENTION: 1000-05-12.656,978
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| FITTE OF INVENTION: 1000
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llarity 100.0%; Pred. No. 7e-10;
Conservative 0; Mismatches 0; Indels (
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61 GTCTGCTTCCCTGTGTGTGGAAGTGCCCTCGGAGAC 98
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3.04; Score 38; DB 10; I
Best Local Similarity 100.08; Pred. No. 7.1e-10;
Matches 38; Conservative 0; Mismatches 0;
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Publication No. US20020160453A1
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Best Local Similarity
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US-10-029-191-22
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; ORGANISM: rat
US-09-997-579-3
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LENGTH: 2220
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Weillock 127-13214 Application US/10027632
Sequence 12314-pplication US/10027632
Sequence 12314-pplication US/10027632
GENERAL INFORMATION: USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF US
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Patent No. US20A204865A1
APPLICANT: Renk, David R.
APPLICANT: Rank, David R.
APPLICANT: Renk, David R.
APPLICANT: Chen, Mensher David R.
APPLICANT: Chen, Mensher David R.
APPLICANT: Chen, Mensher BROWNE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
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APPLICANTON WEBLOO FOR Identifying Modulators Of Ion Channels
FILE REPRENCE: PRI-0000 (ORT 1534)
CURRENT APPLICANTON WINSER: V8210/121,759
CURRENT FILING DATE: 2002-06.26
NOWHER OF SEQ ID NOS: 20
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                                          Sequence 20, Application US/10121759
Publication No. US20030194751A1
GENERAL INFORMATION:
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US-10-121-759-20/c
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LENGTH: 24
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Query Match 1.7%; Score 22; DB 9; Length 462; Bast Local Similarity 100.04; Pred. No. 0.36
Matches 22; Conservative 0; Mismatches 0; Indels
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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SEQ ID NO 15643
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OTHER INFORMATION: EXFRESSED IN LUNG, SIGNAL = 1.3
US-09-864-761-15643
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PRICOR PILING DATE: 2001-01-10 (2018)
                                              FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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TITLE REFERENCE: 0713-0320-0320

CURRENT PLING DATE: 2000-011-13

FRIOR PILICATION NUMBER: 06/112,511

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1.6%; Score 20; DB 10; Length 2517;
Bet Local Similarity 10:0%; Pred. No. 4.1;
Bet Conservative 0; Manacches 0; Indels 0
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US-09-712-363-4
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                  Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
; LOCATION: (266)..(2782)
US-10-219-219-3
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LENGTH: 2884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.7%; Score 21; DB 12; Length 621; Best Local Similarity 100.0%; Pred. No. 1.3. Matches 21; Conservative 0; Mismatches 0; Indels
BRIOR PELLING MWBRR. 18 60/198,676

BRIOR PELLING MARS. 2000-64-20

BRIOR PELLING MWBRRS. 18 60/193,483

BRIOR PELLING MWBRS. 18 60/193,483

BRIOR PELLING MWBRS. 18 60/185,218

BRIOR PELLING MATE. 2000-02-24

BRIOR PELLING MWBRS. 18 60/167,363

BRIOR PELLING MWBRS. 18 60/167,363

BRIOR PELLING MWBRS. 198 60/167,363

REGOR PELLING MATE. 1999-01-23

REGOR PELLING MWBRS. 1986-06-19

REGOR PELLING MATE. 1999-06-19

REGOR PELLING MATE. 1999-06-19

SOFFWARE. PREASED FOR MINGORN 18 60/146,002

REGOR PELLING MATE. 1999-08-19

SOFFWARE. PREASED FOR MINGORN WERSION 4.0

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US-09-712-363-4/c
; Sequence 4, Application US/09712363
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US-10-027-632-132914
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LENGTH: 621
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Gaps ö

us-09-936-680-4.olig10.rnpb

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Length 471;
                        0; Indels
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = US-09-864-761-679
             Query Match 1.5%; Score 19; DB 9;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches
                                                       Search completed: December 6, 2003, 01:54:59
Job time : 497 secs
                                 521 TGAAGAGAGAGGAGGTGGA 539
                                       209 TGAAGAGAGAGAGGTGGA 191
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                                500 AGCTGCGCTGCATCTCCTGC 519
         347 AGCTGCGCTGCATCTCCTGC 328
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December 5, 2003, 17:21:16; Search time 20.95 Seconds (without alignments) 5014:271 Million cell updates/sec
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1. (sgm2.6/pcdata/l/ina/SA, COMB.seq.*

1. (sgm2.6/pcdata/l/ina/Sa. COMB.seq.*

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    569978 segs, 220691566 residues
                                                                                                                                                                                                                                                  US-09-936-680-4_COPY_1024_1261
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                                                                                                 OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                               Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	e 14,	14	14,	14	Sequence 3, Appli	Sequence 19, Appl	Sequence 19, Appl	~	156	ø,	20	20	Sequence 32, Appl	Sequence 32, Appl	m	ñ	æ	97	Sequence 17, Appl	ó	20	ř	Sequence 40, Appl	Sequence 30, Appl	Sequence 20, Appl	Sequence 21, Appl	Sequence 22, Appl
SUMMARIES		ID	US-08-232-463-14	US-08-961-810-14	US-08-352-902D-14	US-09-265-503B-14	US-09-741-154-3	US-09-030-156-19	US-09-645-757-19	US-09-056-226-1	US-08-927-219-126	US-08-332-766A-9	US-09-030-156-20	US-09-645-757-20	US-09-007-005-32	US-09-244-796-32	US-09-007-005-3	US-09-244-796-3	US-09-341-587-8	US-09-128-155-16	US-09-128-155-17	US-09-171-162B-9	US-09-171-1628-10	US-09-358-972-136	US-09-406-065-40	US-09-383-316-30	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22
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		Match Length DB	7218	526	526	526	16389	74	74	3693	6254	367	78	78	248	248	277	277	3166	152331	176373	54	54	70	70	70	246240	246240	246240
		Match	15.2	14.3	14.3	14.3	13.7	13.4	13.4	13.4	13.4	13.2	13.1	13.1	12.9	12.9	12,9	12.9	12.9	12.9	12.9	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8
		Score	36.2	34	34	34	32.6	31.8	31.8	31.8	31.8	31.4	31.2	31.2	30.8	30.8	30.8	30.8	30.8	30.8	30.8	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4
	Dogwalt	No.	-	0	3	0	S	o o	0 7	80	6	c 10	c 11	c 12	c 13	c 14	0 15	o 16	17	c 18	19	20	c 21	~	c 23	N	25	36	27

15.2%; Score 36.2; DB 1; Length 7218;

Query Match

TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear IMMEDIATE SOURCE: CLONE: pTZgpt-F18 US-08-232-463-14

Sequence 13, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 121, Appl Sequence 151, Appl S		
PCT-US91-06251-23 Seary US-05251-23 Seary US-05-29-3331-1 Seary US-05-29-331-1 Seary US-05-22-291A-8612 Seary US-05-22-291A-8612 Seary US-05-22-291A-8612 Seary US-05-22-291A-8612 Seary US-05-238-376-515 Seary US-05-338-376-516 Seary US-05-338-376-516 Seary US-05-338-376-516 Seary US-05-338-376-516 Seary US-05-338-376-516 Seary US-05-338-376-517 Seary US-05-3393A-14 Seary US-08-844-188-14	ALIGNMENTS 1. US/0822463 1. CSR. P. P. G. R. SALIGNMENT FOWLECK VIKUS 1. SALIGNMENANT FOWLECK VIKUS 1. SALIGNMENANT FOWLECK VIKUS 1. SALIGNMENANT FOWLECK VIKUS 1. SALIGNMENANT FOWLECK VIKUS 1. SALIGNMENT FOWLECK	
200 200 200 200 200 200 200 200 200 200	DORNIER, ESCHEILLIN CONTROL CO	QUENCE CHARACTERISTICS: LENGTH: 7218 base pairs
00 00000000000000000000000000000000000	PREGILT 1 108-08-22-46-14 SEQUENCE 14, A. PERICANT: CREEKAL INFORM APELICANT: APELICAN	SEQU 1.

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APPLICANT: Lisky, Robert M.
Bromer, C. Brid
Baker, Sean M.
Baker, Sean M.
Boldag, Renic, Richard D.
Folodher, Richard D.
MISPATION: COMPOSITIONS AND METHODS RELATING TO DNA.
MISPATION TO REPLAIN GRADE
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ADDRESSEE: Kolisch, Hartwell, Dickinson, McCormack &
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APPLICANT: Bronder, C. Eric
APPLICANT: BAKEN Sean M.
APPLICANT: BAKEN Sean M.
APPLICANT: BACHORING Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rolling Rollin
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COMPUTES: IRM PC COMPACTION OF COMPACTION OF COMPACTION OF COMPACTION OF COMPACTION OF COMPACTION OF COMPACTION OF COMPACTION NUMBER: US/06/352,902D CLASSIFFORTION: CURREN OF COMPACTION OF COMP
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 224-6655
TELEFAX: (503) 295-6679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
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                                                                                                                                                                    US-08-352-902D-14/c
; Sequence 14, Application US/08352902D
; Patent No. 6191268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heuser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 97204
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                  RESULT 3
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                                                                                                                                                                                         1035 GAGCTTGGCTGCAGGTCGAGGGAGCTTGCGATYYYYYXYXYXYXYXYXYXYXYXYXYXYXYX 1094
                                                                                                                                                                                                                                                                                                       80 GGAGGGGCCCCCAAGGGCCCCCATCCCTTCCATGCATCCATTGTTCTGTTCAT 139
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                                                                                                                                  20 GAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCA 79
                                                0; Gaps
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APPLICANT: Baker, Sen Mr.
APPLICANT: Baker, Sen M.
APPLICANT: Baker, Sen M.
APPLICANT: Bolds, Rond, J.
APPLICANT: Molodine, Nicheld D.
APPLICANT: Molodine, Nicheld D.
APPLICANT: Molodine, Nicheld D.
APPLICANT: Molodine, Misbarca Respanse, Sen Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarca Respanse, Misbarc
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      Best Local Similarity 8.4%; Fred. No. 0.023; Matches 17; Conservative 109; Mismatches 77; Indels
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STREET: 520 S.W. Yamhill Street, Suite 200
CITY: Portland
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PatentIn Release #1.0, Version #1.25
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REGISTRATOR NUMBER: 33,557
REGISTRATOR NUMBER: 036,557
PELECOMMUNICATION INFORMATION: 0569
TELEFORM (503) 24,4655
TELEFORM (503) 255-6679
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APPLICATION NUMBER: US/08/961,810
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Patent No. 6165713
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 526 base pairs
TYPE: nucleic acid
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MOLECULE TYPE: DNA (genomic)
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MEDIUM TYPE: Floppy
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Matches 40; Conservat
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NUMBER OF SEQUENCES:

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TITLE OF INVESTION: WETHORS AND APPRACTUS FOR DETERMINATION OF LENGTH
TITLE OF INVESTION: WETHORS AND APPLACED AS TO USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF USE OF US
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Sequence 15, Application US/09030156
Sequence 15, Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control Control
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APPLICANT: Colsamit, Joseph J.
TITLE OF INVENTION: Contract, of Fioral Induction in Plants
TITLE OF INVENTION: and Uses Therefor
TITLE OF INVENTION: and Uses Therefor
CURRENT FILE DEPENTOR: NUMBER: US/09/056,268
GURRENT APPLICATION NUMBER: US 09/000,640
ENALIZE APPLICATION NUMBER: US 09/000,640
ENALIZE APPLICATION NUMBER: US 08/000,144
ENALIZE APPLICATION NUMBER: US 08/000,144
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Patent No. 6395493
GENERAL INFORMATION:
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Patent No. 6177614
GENERAL INFORMATION:
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Best Local Similarity 76.5:
Matches 39; Conservative
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US-09-030-156-19
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                  SEE: Kolisch, Hartwell, Dickinson, McCormack & Heuser: 520 S.W. Yamhill Street, Sulte 200
Portland
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MEDIUM TUBE: PLODPY disk
MEDIUM TUBE: PLODPY disk
OPERATURG SYSTEM: PC-DOS/MS-DOS
OFFRARE: PECENTRY Release #1.0, Version #1.25
GURRERN APPLICATION DATA:
FILING DATE: MRTGR. 10, 1999
FILING DATE: MRTGR. 10, 1999
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INPORMATION POR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 526 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-265-503B-14
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 58.9%
Matches 56; Conservative
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CORRESPONDENCE ADDRESS:
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Best Local Similarity
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105 CTTCCCTTCATGCATCCATTGTTCTTTCATTCATTCATCCATACATCCACCTGCTCT 163
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LOCATION: 1287. 4273
OTHER INFORMATION: /note= "N = A or G or C or T"
US-08-927-219-126
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Sequence 9, Application US/08332766A

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APPLICATION NUMBER: US 60/028,056
PILLING DATE: 02-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/025,719
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                                                                                                       US 60/029,679
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2.TP: 2006-3348
COMPUTER READABLE FORM:
MEDIUM TYPE: F. LADAPY disk:
COMPUTER: IN PC COMPUTER:
OPERATING SYSTEM: PC-DOS/NS-DOS
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TELEMONICATION INFORMATION:
TELEMONICATION INFORMATION:
TREATMENT 312/416-300
INFORMATION FOR 8EQ 1D NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 6754 Dase pairs
TITES: MILLSIGH SAID
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 30-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,3
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13.4*; Score 31.8; DB 3; Length 3693;
Bast Local Similarity 77.2*; Fred No. 0.54;
Bast Local Similarity 77.2*; Pred No. 0.54;
Matches 42; Conservative 0; Mismatches 17; Indels 0;
Matches 42; Conservative 0; Mismatches 17; Indels 0;
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COMPUTER READLE FORM,
COMPUTER: IEM PC compatible
COMPUTER: STSTEM: PC-2006/MS-DOS
SOFTWARE: Parentlin Release #1.0, Version #1.30
APPLICATION DASH: US (06/927,219)
Concurrently Herewith
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INFORMATION: n = A, T, C or G
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Patent No. 6187533
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; OTHER INFORMATION: n = A,T,C or G
US-09-056-226-1
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LOCATION: (241)...(329)
OTHER INFORMATION: intron
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INFORMATION: intron
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LOCATION: (921)...(2347)
OTHER INFORMATION: intron
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
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LENGTH: 248
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LENGIH: 248
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Sequence 20. Application US/09645757

Patent No. 6295433

GREERAL, IRCORANTON: SOBOROWSKI, SORDAL G.

TITLE OF INVENTION: PATFOCK AND APPARATUS FOR DETERMINATION OF LENGTH

TITLE OF INVENTION: PATFOCK SERVINGER UNDAR

FILE REFERENCE: DAVID 8. MUREHY: Nanogen 256/229

CHRENT FILING DATE: 2000-08-24

CURRENT FILING DATE: 2000-08-24

SOFTHARE: PLENGTH 1000-08-24

SOFTHARE: PLENGTH 1000-08-24

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MOLECULE TYPE: DNA (genomic)
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                            LENGTH: 367 base pairs
TYPE: nucleic acid
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ORGANISM; Homo sapiens
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LENGTH: 78
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| APPLICANT SCOREA, Jack W. APPLICANT SCOREA, Jack W. APPLICANT SCOREA, Jack W. APPLICANT SCOREA, Jack W. APPLICANT SCOREA, Jack W. APPLICANT SCOREA, SIGHT W. TITLE OF INVENTION: FUSIONS | TITLE OF INVENTION: FUSIONS | TITLE OF INVENTION: FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | FUSIONS | 
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        30; Indels
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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December 5, 2003, 23:19:13; Search time 441 Seconds (without alignments) 7718:801 Million cell updates/sec Run on:

OM nucleic - nucleic search, using sw model

US-09-936-680-4 Perfect score:

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Pred. No. is the number of results predicted by chance to have a core greater than or equal to the score of the result being printed, and is derived by analysis of the cotal score distribution.

SUMMARIES

	Description	Human beta3 cDNA.	Human signal trans	Human novel sodium	Human EST-derived	Human polynucleoti	DNA encoding novel	DNA encoding novel	EST clone BM4. Ho
	Ω	AAC67837	ABA93727	AAF84146	AAH98320	AAK52345	AAS86764	AAS86763	AAV86895
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	Que <i>ry</i> Match Length DB	1261	4052	1510	978	1045	1195	3531	471
do	Query Match	100.0	87,5	68.2	63.3	62.4	31,4	31,0	25.7
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	Human reproductive	Human testicular a	Human voltage-gate	Human polynucleoti	Human polynucleoti	Rat sodium channel	beta3 8	Rat sodium channel	Rat sodium channel	Human reproductive	Human testicular a	Human novel betai-	Human genome-deriv	Villin gene promot	Human immune/haema	Human endogenous r	Mycobacterium tube	Human foetal cDNA,	Mycobacterium tube	Wild-type bacteria	Human immune/haema	Human immune/haema	Mycobacterium tube	Mycobacterium tube	foet				#701	#712			Human genome-deriv	Rat CRF2-alpha rec		Rat corticotrophin
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ALIGNMENTS

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AAC67837 standard; cDNA; 1261 BP.
                                                                   (first entry)
                                                                15-FEB-2001
                              AAC67837;
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RESULT 1

Human beta3 cDNA.

Human, bee sub-unit; beta; analgest; anticovolus absorbit; correbroprovestive, vescuropic; cardiant; neotropic; cytostitic; dermaclogical; gene therapy, voltage-stated sodium channal; pain; elanigation to recover sections in the section of sections and the section of sections and the section of correct sections and the section of correct sections and correct sections are consistent paragonal sections.

Homo sapiens.

WO200063367-A1. 26-0CT-2000. 24-FEB-2000; 2000WO-EP01783.

99US-0129473. 15-APR-1999;

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Dixon A, Jackson A, Morgan K; Cox P,

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GGCAGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCT GGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTG GECCTCTACACCTGCAATGTCCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTG AAGACGACGCGGCTGATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCT AAGACGACGGCTGAATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAAGACTTCACCTCT GTGGTCTCAGAAATCATGAAGTACATCCTTCTGGTCTTCCTCACCCTGTGGCTGCTCATC 841 GIGGICTCAGAAAATCAIGAAGTACATCCTTCTGGTCTTCCTCACACCTGTGGCTGCTCATC 901 GAGATGATATATTGCTACAGAAAGCTCTCAAAAGCCGAAGAGGCAGCCCAAGAAAAGGC TCTGACTACCTTGCCATCCCATCTGAGAACAAGGAGAACTCTGCGGTACCAGTGGAGGAA TAGAACAGGAGCAGTGTGACATGAGGTGGCCTGAACACCTGAGGGACTGGACATCCCATG TTCAGCAATGTCAATGCCATCAGGAGGCGCCCCAAGGGCCCCCATCGCTTCCTTGC

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                                                                              Novel nucleic acids encoding a beta-1 subunit from a voltage-gated sodium channel, and their corresponding polypeptides, useful for detecting and treating sodium channel-associated conditions, e.g. pain,
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                                                                                                                                                                               Claim 10; Page 70-71; 88pp; English.
                                                                                                                                           spilepsy and stroke
                   2000-665241/64
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Best Local Similarity
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CGCCAGCCCCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCCTCGTGCTT

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brain; foetal kidney; melanoma; testis; amygdala;
                                                                                   Human signal transduction cDNA clone amy2_2f18.
                                                                                                                                                                                                    (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                       86
                                      ABA93727 standard; cDNA, 4052
                                                                                                                                                                       25-APR-2001; 2001WO-IB02050.
                                                                                                                                                                                     25-APR-2000; 2000US-199380P
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                                                                                                                         Homo sapiens.
                                                                   30-APR-2002
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                    RESULT 2
ABA93727
ID ABA9
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WPI; 2002-055860/07.

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Human cDNA sequences and clones derived from human fetal brain, fetal ktüney, melanoma, teetis and amygdala cDNA libraries, useful in genetic screening and therapy.
                                                   Claim 1; Page 174-175; 611pp; English
P-PSDB; ABB05689.
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The present intrention describes seemallages and computer readable media offectal brain, fortal kindray, malanama, testis and amydala comba fortal brain, fortal kindray, malanama, testis and amydala comba libraries. ABA93702 to ABA93705 represent human cDNA sequences from the present invention which encode the proceins given in ABB06520 to ABB06729. The human cDNA sequences and clones can be used in sequences and clones can be used in gene example they may be used in a variety of applications; for example they may be used in prefit as a variety of applications; for comba first assets the man generic material for implementing large-scale screening strategies and for treating diseases via gene therapy procedures.

Sequence 4052 BP; 994 A; 1033 C; 1036 G; 989 T; 0 other;

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                                                                                                                                                       GGCCCCCGGAGCGGCTCGTTCGGCTCCCTCGAACTGGGGAGGTCCCAGTGGGGTCGCTTAGGG
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                                                                                                                                                                                                                                                                                                                                                          CCAGCCCCAGAAGATGCCTGCCTTCAATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                            CTACTGGGTCAGTGTCTGCTTCCCTGTGTGTGTGCCCTCGGAGACGGAGGCCGT
                               0; Gaps
87.5%; Score 1104; DB 24; Length 4052;
99.8%; Pred. No. 0;
.ive 0; Mismatches 3; Indels 0;
               Best Local Similarity 99.8%;
Matches 1254; Conservative
                                                                                                                                                       123
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     Query Match
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                                                                                                                                                                                                                                                         243
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7.23 CCTCPACACTICCARGAGATTAGACTAGAGCATCAGCATCAGCATTAGAGCATCAGCATTAGAGAGCATTAGAGAGCATTAGAGAGAG

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Human novel sodium channel betal-like subunit encoding CDNA.
                       AAF84146 Btandard; cDNA; 1510 BP
                                                                                                         (first entry)
                                                                                                         07-SEP-2001
                                                                  AAP84146;
AAF84146
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Sodium channel; sensory neurone specific channel; betal-like subunit; SNS; therapeutic; pain; analgesic; ss. /*tag= a /product= "sodium channel betal-like subunit" Location/Qualifiers 213..860 WO200144293-A2 Homo sapiens Key

Sanseau P; 14-DEC-2000; 2000WO-GB04802 99GB-0029970 (GLAX) GLAXO GROUP LTD Plumpton M, Powell AJ, WPI; 2001-398129/42 P-PSDB; AAB85206 17-DEC-1999; 21-JUN-2001

Novel sub-unit for voltage-gated sodium channel proteins for producing

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1189 GCTTTCACCTCTGACTCCCTAACTCCATCAGGCTCTAGGCACATAAGACTCTGCCAGA 1248
                                             1026 GCTTTCACCTCTGACTCCCTAACTCCATCAGACCTCTACGCACCATAAGACTCTGCCAGA 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 CTCGAACTQGGGAGGTCCAGTGGGGTCGCTTAGGGCCCAAAGCCCCCACCCGGCTCCAAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 GGCGACTGTCCGTGGTGCTGAGCGCCGGCGAGAGCGGGCGCGGCGGCGGCTGATCGGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomakey, longy sea utvinin; expressed sequence tag; EST; diagnostics; foremaic test; gene apping; genatic disorder; blodiversity; qene therapy; nutrition; 88.
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                                                                                                                                                                                                                                                                                                                                                                        AAH98320 standard; cDNA; 978 BP.
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03-AUG-2000; 2000US-0631451.
15-SEP-2000; 2000US-0663870.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  798; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                          The invention provides a novel heart-like suburust for voltage-gated sedium in channel polypeptide, specifically a sensory neurons specific channel (1895) aubunit. The provel betal-like subunit is useful for producing a therapeutic agent which is useful treating pain in a patient. The subunit can be expressed by standard recombinant meshoology. The present sequipes registers a funant movel action to have been expressed to the subunit can be expressed by standard recombinant meshoology. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         786 CAAGAAACGCGCTCTGACTTGCCATCCCATCTGAGAACAAGGAGAACTCTGCGGTA 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  846 CCAGTGGAGGAATAGAACAGGAGCAGTGTGACATGAGGTGGCCTGAACACTGAGGGACT 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            906 GGACATCCCATGTTCAGCAATGTCAATGGCATCAGGAGGGGGCGCCCAAGGGGCCCCAATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 860; DB 22; Length 1510;
Pred. No. 0;
0; Mismatches 1; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                             Sequence 1510 BP; 350 A; 410 C; 414 G; 336 T; 0 other;
                                                       Claim 4; Page 29-30; 31pp; English.
agents useful for treating pain
                                                                                                                                                                                                                                                                                                                                                                                                                                               68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.94;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.99
Matches 910; Conservative
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The invention relates to polymuclaonides (AAKS1455-AAKS1435) and the encoded by relates to polymuclaonide the chibit activity elating to optokine polypetides (AAKS131-AAMS1012) that enclose the chibit activity elating to optokine so ell differentiation or which may induce product to cher optokines in other ell populations. The product borides and polymetides are useful in gene therapy, accines or peptide therapy. The polypetides have various eyochine-like activities, activity immunocollatory excitities, activity in an extra production of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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                                                                                                                                                                                                                                                                                                Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 787; DB 22; Length 1045;
                                                                                                                                                                                Liu C, Drmanac RT, Asundi V, Zhou F, Xu C, Ca
Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Wang Y, Welhrman T, Goodrich R;
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0; Mismatches
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               2000US-0560875.
2000US-0598075.
2000US-0620325.
2000US-0654936.
2000US-0663561.
2000US-0693325.
2000US-0728422.
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Best Local Similarity 99.9%;
Matches 837; Conservative (
2000US-0496914
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             27-APR-2000; 2
20-JUN-2000; 2
19-JUL-2000; 2
01-SEP-2000; 2
15-SEP-2000; 2
20-OCT-2000; 2
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Zhao QA,
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                                                                                                                                                                                                                             CCTGGGGGCAGTTCGTCCCAAAGGGTTTCCTCGAAAGAATCTGAGAGGGGGGCAGTCCTTG
                                                                                             CTGGGGGCCAGTTCGTCCAAGGTTTCCTCGAAGAATCTGAGAGGCGCAGTCCTTG
                                                                                                                                       AATAGATTGTTTCCCCTGGCTTCTCTCGTGCTTACTGGGTCAGTGTCTGCTTCCCT
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                                                                                                                                                                                                                                                                                                                                                                             GTCTCAGAAATCATGATGTACATCCTTCTGGTCTTCCTCACCTTGTGGGCTGCTCATCGAG 829
                                                                                                                            AGCAAGGACCTGCAGGACGTGTCCATCACTGTCAAGGTCACTCTGAAGGACTCTGGC 723
                                                                                                                                                                                                     CTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCCATCGGCCCTTTGTGAAG 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGATATATTGCTACAGAAAGGTCTCAAAAGGCGGAAGAGGCCCAAGAAAAGGGGT 887
                                                       TATCGGAATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCTGCAGTGGAATGGC
                                                                              TATCGGAATGCCACCACCAGGAGGTGGAGAGCCCCTTTCAGGGGGGCCCTGCTGGAATGGC
                                                                                                                                                                  AGCAAGGACCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACTCTGAACGACTCTGGC

    chromosome mapping; gene mapping; gene therapy; forensic;
supplement; medical imaging; diagnostic; genetic disorder; ss.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polymucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #22568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 22568; 103pp; English.
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23-AUG-2000; 2000US-0649167.
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(III). (III) is useful for exercating antibodies against it, detecting or quantitating a polypeptide in tissue ase molecular weight markers and as food supplement. (III) and its hinding partners are useful in medical imagina of eitee expressing (III). (I) and (III) are useful for treating disorders involving aberrant protein expression to biological activity. The polypeptide and polymucleotide sequences have applications in the advantage and to produce other types of data and produces dependen on DNA and a proceeding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic formst directly from MIPO at the properties of the bacterial of the content of the printed specification, but was obtained in electronic formst directly from MIPO at the properties of the intercent of the printed specification, but was obtained in electronic formst directly from MIPO at the part of the properties of the intercent of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the prin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 GTGGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         730 ACCTGCAATGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCTGATCCCCCTAAGAGTCACCGAGGAGGAGTGGAGGAGTTCACCTCTGTGGTCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   881 CGGCTGATCCCCCTAAGAGTCACCGAGGAGGCTGGAGAGGACTTCACCTCTGTGGTCTCA
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food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1195;
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                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 1195 BP; 253 A; 356 C; 381 G; 205 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoding novel human diagnostic protein #22567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.5e-182;
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941 GAAATCATGATGATGTACATCCTTCTGGTCTTCCTCACC 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 396; DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                31.4%; Scc. 100.0%; Pred. No. 2...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sest Local Similaricy ......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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AAV86895 standard; cDNA; 471 BP.

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(HYSE-) HYSEO INC.

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The invention relates to isolated polymuchotide (1) and propertide (11) experience (127) Kingerid and the repercence (127) Kingerid and for intronceme polymerical chain read in read-in read-in read-in recording the control of the relationship of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1079 GTGGTGGAATGGTTCTACAGGCCCGAGGGCGGTAAAGATTTCCTTATTTACGAGTATCGG 3138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3259 ACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACGACG 3318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              610 AATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCGCCTGCAGTGGAATGGCAGCAAG 669
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                                                                                                                                                New isolated polynucleotide and encoded polyneptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
blodyversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 391; DB 23; Length 3531;
Pred. No. 6.78-180;
0: Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3531 BP; 952 A; 901 C; 960 G; 718 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.0%; suc. No. c. 100.0%; Pred. No. c. 0; Mismatches
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                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 22567; 103pp; English.
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.0
Matches 391, Conservative
Drmanac RT, Liu C,
                                                                WPI; 2001-639362/73.
                                                                                              P-PSDB; ABG22576
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The sequence represents an expressed sequence agg (EST), and is a polymore expresents an expression are polymore or the suverion are all secreted EST sequences and proceins expressively of human transcending the sequences and proceins enrolled from a vortice of the predicted to have useful biological activities which would make the man predicted to have useful biological activities which would make the maintain and animals. Although no supporting date is given suggested scrivities and the matrix almans are refinal thing or suppressing activity. Hematoposess regularing activity, femerate (Chemofinice activity, hamened and think matrix producting processing activity, reseapor/ligand activity, hamened activity and through the activity reseapor/ligand activity, and activity, hamened activity and through the sequences are also stated to be useful for gone districts.
                                                                                                                              tissue growch, activin inhibin; tumour invasion suppressor; EST, human; chemcaxis; chemchisis, hamenesasis; gene therapy; thrombolysis; ecceptor; lispani; anti-nifammatory; tumour inhibitor; de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 GGCAACCCCATGAAGCTGCGCTGCATCTCCTGCATGAAGAGAAGAAGGAGGTGGAGGCCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   547 ACGGIGGIGGAAIGGITCIACAGGCCCGAGGGCGGIAAAGAITICCITAITTACGAGTAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polymucleotides encoding human secreted proteins - derived from e.g. human blood, Kidney, foetal lung, placenta, restes, brain, ovary, plutitary, retina and colon cDNA libraries
                                                                                                                 Expressed sequence tag; secreted protein; haematopoiesis regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.7%; Score 324; DB 20; Length 471; Best Local Similarity 10.0%; Ped. No. 2.0e.4% Masches 334; Conservative 0; Mismatches 0; Indels 0
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Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 471 BP; 93 A; 126 C; 143 G; 108 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 383-384; 633pp; English.
                                                                                                                                                                                                                                                                                                                                    98WO-US06954.
                                                                                                                                                                                                                                                                                                                                                                          97US-0835913.
                                     27-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   (GEMY ) GENETICS INST INC.
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Spaulding V,
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                                                                           EST clone BM4.
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RESULT

Query Match

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22-AUG-2000;

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The invention relates to Asolated polymucleotide (I) and probes, polypeptide (II) as useful is a merital as hybridisation probes, polypeptide (II) sequences, (II) is useful it as hybridisation probes, and for chromosome and gene seapens as also used illuig production of (III). The characteristic sequences also used illuight production of (III). The characteristic sequences and (II) are treat disease afterey inchingues to reserve normal activity of (III) or to treat disease afterey inchingues to reserve normal activity of (III) or to treat disease afterey inchingues (III). (III) and (III) or to treat disease afterey inchingues (III) or contain a molecular view inchingues (III) or questification of quantitating a polypeptide in tissue, as molecular viewing inchingues (III) in and (III) are assets in for treating disorders involving aberrant procein expression or biological activity. The polypeptide and polymucleotical sequences have applications of adjacential or general disorders of other traiter to assess biodiversity of any or produce other types of data and produce dependent on DNA and dance in the procession of the invention.

Construction of the contained of the invention.

Construction of the invention.

Construction of the invention.

Construction of the invention.
                        379 TACACCTGCAATGTGTCCCGGGAGTTTGAGGCGCATCGGCCCTTTGTGAAGACG 438
727 TACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCTTTGTGAAGACG 786
                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polymuclocitie and encoded polypeptides, useful in 
admonstrate. Accemics, gene mapping, identification of mutation 
responsible for genetic disorders or other traits and to assess 
bicolyperity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 621 BP; 156 A; 155 C; 175 G; 135 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #22566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 22566; 103pp; English.
                                                                                810
                                                                                                  ACCCGCTGATCCCCCTAAGAGTC 462
                                                                             787 ACGCGGCTGATCCCCCTAAGAGTC
                                                                                                                                                                                                                 AAS86762 standard; cDNA; 621 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT;
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23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                               (first entry)
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                                                     58 ATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCCCCTGCAG 117
                                                                                     714
                                                                                               715 GACTCTGGCCTCTACACCTGCAATGTGTCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCC 774
                                                                                                                                       178 GACTCTGGCCTCTACACCTGCAATGTGTCCCCGGGAGTTTGAGTTTGAGGCGCATCGGCCC 237
                                                                                                                                                                                                                                                                                                                                Human; reproductive system related antigen; reproductive system disorder;
                                                                                655 TOGRATGGCAGGCCTGCAGGACGTGTCCATCACTGTGCTCAACGTCACCTCTGAAC
                    Gaps
                                        595 ATTTACGAGTATCGGAATGGCCACCAGGAGGTGGAGAGCCCCTTTCAGGGGCCCCTGCAG
                     ..
                                                                                                                                                                                                                                                                                                           Human reproductive system related antigen DNA SEQ ID NO: 7659.
          Pred. No. le-95;
; Mismatches 0; Indels
                                                                                                                                                                    775 TITIGIGAAGACGACGCGCTGATCCCCCTAAGAGTCAC 812
                                                                                                                                                                                   238 TTTGTGAAGACGCGGCTGATCCCCCTAAGAGTCAC 275
100.0%; Pre-
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2000US-0214886.
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2000US-0218290.
2000US-0220963.
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                    218; Conservative
                                                                                                                                                                                                                                                                                                                                          cancer; gene therapy; ds.
        Best Local Similarity
Matches 218; Conserv
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17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
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07-7UL-2000;
11-7UL-2000;
11-7UL-2000;
14-7UL-2000;
26-7UL-2000;
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14-AUG-2000;
14-AUG-2000;
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2000005-023043
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22-AMG-2000 22-AMG-2000 22-AMG-2000 23-AMG-2000 20 21-AMG-2000 20 21-AMG-2000 20 21-AMG-2000 20 25-2000 20 25-2000 20 25-2000 20 25-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 20 26-2000 20 26-2000 20 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-2000 20 26-200
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The present invention provides the protein and coding sequences of a number of bunnar reproductive system related aniques. These can be used in the presention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a procesh of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCCATGTTCAGCAATGTCAATGGCATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4625 BP; 1222 A; 1130 C; 906 G; 1367 T; 0 other;
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17-80V-2004) 200018-043908
17-10V-2004) 200018-043908
17-10V-2004) 200018-043111
17-10V-2004) 200018-043111
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2000US-0251989.
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2001US-0259678.
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2000US-0246477.
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2000US-0246528.
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2000US-0246610.
2000US-0246611.
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29-SEP-2000;
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      Human; testicular antigate; testes; caroct; matestasis; sumumu discorder; reproductive system discorder; urinary system discorder; gene thearpy; cardiovascular discorder; respiratory discorder; neurological discorder; gene thearpy; gastrointestinal discose; infection; cyrostatic; gene; ds.
                                                                                                                                           Human testicular antigen encoding DNA fragment SEQ ID NO: 2516.
A MEL97864

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B Human LestCullar antigen encoding

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eell culture, drug orcenning gemic hierapy; anti-inflamantory; antiatenhamics, antiatrhitic; hamenetatic; antiatreciosherocic; optostatic; osteopathic; viaostropic, cardiant; virucide; antibacterial; antifungal; vulnerapy; antiulocu; se.

reqeneration; wound healing; infection; immune disorder;

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1044 AGGTGGCCTGAACACCTGAGGGACTGGACATCCCATGTTCAGCAATGTCAATGGCATCAG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1104 GAGGGGCCCCAAGGGCCCCATCGCTTCATGCATCGATCTGTTCTTCATT 1163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 CATCCATACATCCACCTGCCTCTGAGCTTTCACCTCTGACTCCCTAACTCCATCAGACCT 212
                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of 973 human testicular antiquens, and frequents of their genemic sequences. The human testicular antiques is the treatment of cardiovacular, urinary spetem, respreductive spetem, immen, respiratory, neurological and agastrointestrail disorders, infections and particularly cancer, sepecially testicular encers. The present sequence is a DNA encoding a protein fragment of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33 AGGTGGCCTGAACACCTGAAGGGACTGGAACATCCCATGTTCAGCAATGTCAATGGCATCAG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                  Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 17.1%; Score 216; DB 23; Length 4625; Bert Local Similarity 100.0%; Pred. No. 2.16-95; Matches 216; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4625 BP; 1222 A; 1130 C; 906 G; 1367 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1224 CTACGCACCATAAGACTCTGCCAGAACTGAGAAGCC 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 CTACGCACATAAGACTCTGCCAGAACTGAGAAGCC 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA08942 standard; cDNA; 407 BP.
                                                                                                                                                                                                                                       Ruben SM;
                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                          2001US-0259678.
                                             2000US-0256719.
2000US-0251479.
                                                                            2000US-0251856.
2000US-0251868.
2000US-0251869.
                                                                                                                            2000US-0251989.
2000US-0251990.
2000US-0250391.
2000US-0251030.
                                 2000US-0251988.
                                                                                                                                                        2000US-0254097
                                                                                                                                                                                                                                                                                                                   useful for preventing,
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                                           05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
01-DEC-2000;
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Human proteins and DNA encoding sequences useful for preventing, teaching or amaliorating a medical condition in a mammalian subject e.g. arthrits and cancer -

fang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49. (HYSE-) HYSEQ INC.

P-PSDB; ABB11698

05-FEB-2001; 2001WO-US03800. 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875.

#0200157188-A2. fono sapiens. 09-AUG-2001 Claim 1, Page 656; 1963pp; English

Sequences ASS1081-ASS12310 represent 1320 novel human notypeptides, and institute also seasons are sequences and recombinant heavereling contributes against the Diversives and recombinant heavereling committees a sequence and recombinant heavereling committees a managed the properties and recombinant heavereling committees assistent the pipperties, and rechods of detertifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby polypeptides of the invention have homology to known proteins, thereby or polypeptides of the invention have homology to known proteins, thereby committees an insight that the polypeptides of the invention have homology to known proteins, thereby or polypeptides of the invention have homology to known proteins, thereby committees an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight that an insight the production has a set of the proposition of the prop ö Human voltage-gated Na channel subunit homologue cDNA, SEQ ID NO:718. (first entry)

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Sequence 407 BP; 120 A; 91 C; 86 G; 110 T; 0 other;
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Human: oytokine; cell porlieeration; cell differantiation growth factor) haematockishis regolation; tissue growth, immunomchiletor; settling thibbin; chemcratis; chemchinesis; rhomobytis; concesses intiving probliecation; metasterals; cancer; tumour; heematopoistic disorder; puppled cell disorder; raphold cell disorder; rathma rathmis chemcratics; chronic haematopy condition; probliecation; rethinopathy; between thill sechamon and proposed problems of the proposed proposed problems are proposed proposed problems.

11-JAN-2002

ő 7.2%; Score 91; DB 22; Length 407; 9.3%; Pred. No. 6.4e-34; ve 0; Mismatches 1; Indel8 99.3%; Best Local Similarity 99.3 Matches 141; Conservative Query Match

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Gaps

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Sequence 407 BP; 120 A; 91 C; 86 G; 110 T; 0 other; were missing at the time of publication.

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The invention relates to polymucleotides (AMCS1456-AMCS3435) and the encoded polypscides (AMMS1823-AMMS0301 that exhibit activity elating to cytochies, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell polatations will perform the polymptides are useful in gene therapy. Vaccines or polymucleotides and polymptides are useful in gene therapy. Vaccines or e.g. seem cell growth factor activity, imanacopolesus regulating activity, interpolation scrivity and may be useful in the diagnosis and/or treamment of context, lower by even may be useful in the diagnosis and/or treamment of context, lower by even disorders, arthitis and sitilament of context lower precom disorders, arthitis and sitilament.
                  230 GCTGGAGAGACTTCACCTCTGTGTGTCAGAAATCATGATGTACATCCTCTCTGGTCTTC 171
                                                             820 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGTACATCCTTCTGGTCTTC 879
                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; seme cell growth factor; haematopolesis; tissue growth factor; mmunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang J, Zhang J, Ren F, Chen R, Wang ZW; Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                     Human polynucleotide SEQ ID NO 2858.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 5033; 6221pp; English.
                                                                                                                                 940 GAGGCAGCCCAAGAAACGCGT 961
                                                                                                                                                      110 GAGGCAGCCCAAGAAACGCGT 89
                                                                                                                                                                                                                                                    AAKS3329 standard; cDNA; 407 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-APR-2000; 2000US-0560975.
0-UN-2000; 2000US-059075.
19-JUL-2000; 2000US-0620325.
01-SEP-2000; 2000US-065936.
15-SEP-2000; 2000US-063561.
20-OCT-2000; 2000US-0633325.
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                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, D
Wang D, Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                       AAK53329;
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AAK53329/c
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820 GCTGGAGAGGACTTCACCTCTGTGGTCTCAGAAATCATGATGTACATCTTCTGGTCTTC 879
                                                                         230 GCTGGAGAGACTTCACCTCTGTGGTCTCAGAATCATGATGTACATCCTTCTGGTCTTC 171
                                                                                                        880 CTCACCCTGTGGCTGCTCATCGAGATGATATATTGCTACAGAAGGTCTCAAAAGCCGGAA 939
                                                                                                                                                                                                                                                                                                                                                        Humani. oytokinis. coll profiferation; coll differentiation; gene therapy; vaccinin, peptide therapy; stem coll growth factor; hasaatopoissis; tissue growth factor; intuminondulatory; cancer; teuksenia, narvous sytem disorders; arthritis; inflammation; set.
                             0, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing disapnesing and treating e.g. leuksemia, inflammation and Namune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13445; 1399pp + Sequence Listing; English.
7.2%; Score 91; DB 22; Length 407;
9.3%; Pred. No. 6.4e-34;
ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 Human polynucleotide SEQ ID NO 13445.
                                                                                                                                                            940 GAGGCCCAAGAAACGCGT 961
                                                                                                                                                                                     110 GAGGCAGCCCAAGAAACGCGT 89
                                                                                                                                                                                                                                                    AAI93385 standard; cDNA; 509 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
                99.38;
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                               latches 141; Conservative
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                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                 AA193385;
      Query Match
                                                                                                                                                                                                                             RESULT 14
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The invention relates to human polynucleotides (AKT9991-AK19981) and the encoded proteins theofonto-Ak1910) that earthly early elating to evroking relation or eal differentiation or which may induce production of other ordorines in other cell polariations which may induce polynucleotides and polypeptides are useful in gene therapy, vaccines or polynucleotides and polypeptides are useful in gene therapy, vaccines or special characteristics, the entity is entity in the entity in the entity in the control of the entity in the control of the entity in the diagnosis and/or extended to cancer, leakaemia, nervous system disorders, arthitis and inflammation.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing

Job time : 447 secs

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                                                                                                                                                          349 AGCTTGGAAGCGCCAGCCCAGAAATGGCTGCCTTCAAAAGATTGTTTCCCCTGGCT 408
436 AGCCTTGAAAAGCGCGCCGCGAAAATGCTGCTGCCTTCAAAAATTGTTTCCCCTGGCT 408
436 AGCCTTGAAAAGCGCGCAAAAAATGCTGCTGCTTCCTAAAAATGTTCCCCTGGCT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the process and coding agentees of the state Scale control and an advance search and state process and process and process. The special code is a state process, and other seasony on preceptive nerve impulsees, in the cerebilishment and endurance of mood, neurodegenerative and alege discorders, and in the control of wateries contraction, including movements such as the heartheast, dispession and vascular rection, including movements such be used in predictive medicine, ecreening and diagnostic assays, and in pharmacogeneatics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New rat sodium channel beta-3 subunit gene isolated from a rat dorsal
reot ganglion cDMA library for use in Ohromosome mapping, forensic
medicine, monitoring clinical trials and therapeutics
                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rat; sodium channel beta3 protein; Alxxa94h5; pain; sleep disorder; neurodegenerative disorder; mood disorder; muscle contraction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rat sodium channel beta3 protein Alrxa94h5 partial coding sequence.
                                                                                Length 509;
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                                                                          Query Match 5.94; Score 74; DB 22; Length 50 Beer Local Similarity 100.04; Pred. No. 1.2e-25; Matches 74; Conservative 0; Mismatches 0; Indels
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                                        Sequence 509 BP; 88 A; 174 C, 176 G; 71 T; 0 other;
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100.0%; Pred. No. 3.8e-08;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                          AAC90601 standard; cDNA; 645 BP.
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Best Local Similarity 100.0:
Matches 38; Conservative
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Search completed: December 5, 2003, 23:33:12

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Sequence 128, App
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-253-008-44
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100.0%; Pred. No. 3.4;
tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lovenberg, Timothy W.
APPLICANT: Liaw, Cher
APPLICANT: Liaw, Chen
APPLICANT: Cityoridatis, Dinitri E.
APPLICANT: Originatis, Dinitri E.
APPLICANT: DeSoura, Exto E.
TITLE OF INVENTION: CORTIONEDIN RELEASING FACTOR 2
TITLE OF INVENTION: RECEPTORS
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REDIDM TYPE: ROUGH disk
REDIDM TYPE: ROUGH disk
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RESEARCH TABLESTERM: TO COMES WELLOW
SOFTWARS: Patentin Release #1.0, Version #1.25
REMENT APPLICATION DATA
REPLICATION NUMBER: US/N8/381,433A
FILHO DATE: 31-AMN-1995
CLASSIFCATION: 435
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ADDRESSER: SCO and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        690068.401C1
                                                                     ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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Sequence 3, Application US/08381433A

Sequence 3, Application US/08381433A

Security No. 2286203

GENERAL INFORMATION:

APPLICANT: Lovenberg, Timothy W.
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NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
                                                                                                                                                                                   20; Conservative
SOFTWARE: Patentin Ver. 2.1
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TOCATION: 216..1449
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Washington
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Matches 20; Conserva
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US-08-381-433A-3
                                                                                              ; CTHER INFORM
US-09-103-840A-1
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                                                   TYPE: DNA
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| Sequence | Like papilication US/09280116A |
| Sequence | Like papilication US/09280116A |
| Patent No. 63349 |
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Applicant Word, Alexander K.C.
Applicant Terry Control H.P.
TITLE OF INVESTION: BOAT 18 A TUNOR SUPRESSOR THAT IS MUTATED IN PROSTATE
TITLE OF INVESTION: BOAT AND OTHER CANCER TYPES
                                                                                                                                                                                **MEPLICANT*** BLI-FE** JOHN M. **
**PEPLICANT*** BLI-FE** JOHN M. **
**APPLICANT*** BROCKET** LOVEDPA M. **
**APPLICANT*** BROCKET** CONTROLLED M. **
**TILLE OF INVENTION: BOH *** PURNO BP WASS SPECTROMETRY WITH POLIMORPHIC DNA TITLE OF INVENTION: BOH *** PURNO BP ***
**TILLE OF INVENTION: BOH *** BROCKET**
**CHERRAP FLINGO BATE: 1988-09-18 (90/457,177 CHERRAP FLINGO BATE: 1988-09-18 (90/45) ***
**SARLIER APPLICATION MARBERS: 6/0-69,415 BARLIER PLINGO BATE: 1997-09-19 ***
**SOFTWARES: PRICE BLINGO BATE: 1997-09-19 ***
**SOFTWARES: PRICE BLINGO BATE: 2.0
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                                        Sequence 128, Application US/09157177
Patent No. 6090558
GENERAL INFORMATION:
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) Sequence 44 Application US/09535008
| Patent No. 6465629
| SERRAL INFORMATION:
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US-09-157-177-128/c
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Best Local Similarity

Matches

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"E-05-02-02A.") Application US/D9023942A
Patent No. 647224.
Patent No. 647224.
Patent No. 647224.
RAPALIANT: (US only) ARTALIS Ton! Marie and HOOPER John David
TITLE OF INVENTION: NOVEL MOLECULES
ANDREAGE OF SEQUENCES: 40.
CORRESPONDENCE JUDIESS:
ADDRESSER: 5400 GANERO LITY PLAZA
CTT: GARBON CTTY PLAZA
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CTTY: GARBON CTTY PLAZA
                                                                                             Ouery Match 1.4%; Score 18; DB 4; Length 1023; Beet Local Similarity 100.0%; Pred. No. 33; Matches 18; Conservative 0; Mismatches 0; Indels Matches
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COMPUTER: LEADING TYPE:
MEDIUM TYPE: PLODPY disk
COMPUTER: LIN RF Competible
OPERATURG SYSTEM: PC-DOS/WS-DOS
OFFWARE: PARENTLE Release #1.0, Varsion #1.25
CURRENT APPLICATION DATA:
PLIJNG DATE: 13-PE-1599
FLIJNG DATE: 13-PE-1599
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                                                                                                                                                                                                                                                                                                                                                        537 CCTTGACCGAGGGAATCT 554
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Matches 18; Conservative
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Parter No. 652195

PAPLICANT: RESIDENCE NO. 10197

PAPLICANT: RESIDENCE NO. 10197

TITLE OF INVESTION: NO. 10197

TITLE OF INVESTION: NO. 10197

CURRENT APPLICATION WHORE: US/09/252, 991A

CURRENT PAPLICATION WHORE: US/09/252, 991A

PALOR PLING DATE: 1999-07-219/252, 991A

PRIOR PLING DATE: 1999-07-219/252, 991A

PRIOR PLING DATE: 1999-07-219/252, 991A

PRIOR PLING DATE: 1999-07-219/252, 991A
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100.0%; Pred. No. 33;
tive 0; Mismatches 0; Indels
FILE REFERENCE: 2318-259
CURRENT PERLICATION WORBER: US/09/535,008
CURRENT PILINE DATE: 2000-03-23
EMBLIER PELICATION WORBER: U.S. 60/125,806
EMPLIER FILING DATE: 1399-03-23
WINGER OF SEQ ID NOS: 77
SOFTMARE: Patentin Ver: 2.0
LENGTH: 713
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US-09-252-991A-9940
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Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-09-535-008-44
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100.0%; Pred. No. 33;
Live 0; Mismatches 0; Indels
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100.0%; Pred. No. 33;
tive 0; Mismatches 0; Indels (
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MEDITIM TYPE, PLODDY disk
COMPUTER: IN FOOTH OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A CONTROLL OF A
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11808 CCAGGGCCTCCCCAGGCA 11791
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Patent No. 6090620
GENERAL INFORMATION:
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TELEPAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                               Best Local Similarity 100, Matches 18, Conservative
                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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: USA
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US-08-781-891-79
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ZIP: 98104-7092
                                      LENGTH: 44453
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S ON GI OBS
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100.0%; Pred. No. 33;
tive 0; Mismatches 0; Indels
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APELCATION MANERS: US/68/178,257
FILIND MANERS: US/68/178,257
FILIND MANER: US/68/178,257
FILIND MANE: US/68/178,257
APELCATION MONERS: PET/GB92/01291
PRIOR APELCATION MANER: CPT/GB92/01291
PRIOR APELCATION MANER: US/GB11.1992
PRIOR APELCATION MANER: US/GB11.1992
APELCATION MANER: US/GB11.1992
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                                      APPLICANT: LIBERGEBEL, MATTHIAS
APPLICANT: LIBERGEBEL, MATTHIAS
PRICANT: STERIBUCHER, ALEXANDRE
TITLE OF INVENTION: PRODUCTION OF POLYALKANOATS
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
                                                                                                                                                                                                                                                                               ADDRESSEE: CUSHMAN, DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
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; Sequence 5, Application US/09146053A
; Patent No. 6399349
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ORGANISM: Chromatium vinosum
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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Matches 18; Conserv
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Patent No. 6515205
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NAME/KEY: UNBUZE
LOCATION: 34077
OTHER INFORMATION: UNKNOWN
NAME/KEY: UNBUZE
LOCATION: 36816
OTHER INFORMATION: UNKNOWN
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LOCATION: 30136
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 30140
OTHER INFORMATION: unknown
                                                                              NAME/KEY: unsure
LOCATION: 12605
OTHER. INFOSMATION: unknown
NAME/KEY: unsure
LOCATION: 12742
OTHER. INFOSMATION: unknown
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WHEN INFORMATION: Unknown
WHEN INFORMATION: Unknown
LOCATION: 42459
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UCATION: 45669
UTBER INFORMATION: Unknown
WHEN INFORMATION: Unknown
LOCATION: 46813
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NAME/KEY: unsuze
LOCATION: 29980
OTHER INFORMATION: unknown
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LOCATION: 31592
OTHER INFORMATION: unknown
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LOCATION: 31205
OTHER INFORMATION: unknown
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COCATION: 31206
STHER INFORMATION: unknown
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LOCATION: 33095
JTHER INFORMATION: unknown
NAME/KEY: unsure
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R INFORMATION: unknown
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LOCATION: 46826
OTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 47291
                                                    OTHER INFORMATION: unknown
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ACATION: 34066
THER INFORMATION:
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LOCATION: 29370
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LOCATION: 29422
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LOCATION: 29979
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LOCATION: 39020
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      LOCATION: 11609
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             APPLICAN: Et., "Chang-En. Obling a Junco Mulligan, John T. Schellenberg, Gerald D. Schellenberg, Gerald D. Schellenberg, Stands AND GBNZ PRODUCTS RELATED TO WERNER'S SYNDROME
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APPLICANT: Fu, Ying-Hui
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NAME/KSY: unsure
LOCATION: 7421
OTHER INFORMATION: unknown
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LOCATION: 7427
OTHER INFORMATION: unknown
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ORGANISM: Homo sapiens
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LENGTH: 87543
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us-09-936-680-4.olig10.rni

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NANE/KEY: unsure
LOCATION: 59235
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATICN: unknown
              NAME/KEY: unsuze
LOCATION: 52786
OTHER INFORMATION: unknown
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LOCATION: 68660
OTHER INFORMATION: unknown
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LOCATION: 68733
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
NAME/KEY: unsure
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OTHER INFORMATION: unknown
NAME/KEY: unsure
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LOCATION: 79134
OTHER INFORMATION: unknown
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LOCATION: 79198
OTHER INFORMATION: unknown
OTHER INFORMATION; unknown
                                                                                                           OTHER INFORMATION: unknown
                                                                                                                       NAME/KEY: unsure
LOCATION: 53384
OTHER INFORMATION: unknown
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NAME/KEY: unsure
LOCATION: 59215
OTHER INFORMATION: unknown
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LOCATION: 63290
OTHER INFORMATION: unknown
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LOCATION: 66614
OTHER INFORMATION: unknown
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LOCATION; 68697
OTHER INFORMATION; unknown
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LOCATION: 68718
OTHER INFORMATION: unknown
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LOCATION: 54684
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69785
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LOCATION: 52787
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LOCATION: 68739
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LOCATION: 86336
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1.4%; Score 18; DB 4; Length 87543;
100.0%; Pred. No. 33;
tive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0
Matches 18; Conservative
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Search completed: December 6, 2003, 01:46:43 Job time: 117 secs

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34862 TTCTGTTCATTCATTCAT 34879
                                                                                                    UG-08-392-678-22

Sequence 22 Application US/08392678

Patent No. 555281

GENERAL INFORMATION:

APPLICANT: Scasbenko, Philip
1149 TTCTGTTCATTCAT 1166
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0; Gaps
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APPLICANT: II, '1-FING
PAPLICANT: II, '1-FING
TITLE OF INVESTION: HAMAN OSTBOCLAST-SPECIFIC AND
TITLE OF INVESTION: HERATED GENES
NUMBER OF SEQUENCES: 34
ADDRESSE: HAMILTON, BOOK, SMITH & Reynolds, P.C.
STREET: TWO MILITIES BOOK, SMITH & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: JBM PC compacifible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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RDSISPARION WRBER: 12,227
RERENDENCONCHI DINOMES: RC92-02
TELEDOMENI CITON INFORMATION:
TELEDOMENI (117) 81-6340
INFORMATION FOR SEQ ID NO: 2:
SEGURICE CHARACTERISTICS:
LENGTHE 139 base pairs
STRANDENESS: double
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CLASSIZCATION DATA.
PRIOR APPLICATION NUMBER: US/08/045,270
FILME DATE: OG APR 1993
ATYORNEY/AGBRY INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,678
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US-08-392-678-22
                                                                                                                                                             STREET: Two Militia Ling CITY: Lexington STATE: Massachusetts COUNTRY: USA ZIP: 02173
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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PR 10-NMY-2001, 2001MJ-0004922.

XX MAILEY JC. Wallace RH, Scheffer IE;

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70 KDFL-IYEYRNGHQEVESP--FQGRLQWNGS---KDLQDVSITVLNVTLNDSGLYTCNVS 123
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                                                                                                                                                                                                                                                                                           10 LASLVLIYWVSVCFPVCVEVPSETEAVQGNPMKIRCISCMKREEVEATTVVEWFYRPEGG 69
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al Similarity 49.7%; Score 471; DB 24; Length 218;
al Similarity 49.7%; Pred. No. 338-36;
106; Conservative 31; Mismatches 69; Indels 8
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                                     Query Match
Best Local Similarity
218 AA;
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